

6FFLSPEAKLQPayes-902-seq1.rag

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2003, 12:57:01 ; Search time 35 Seconds  
(without alignments)  
53.300 Million cell updates/sec

Title: MAYES-902-SEQ1  
Perfect score: 70  
Sequence: 1 gseflepeaklqpr 14

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SID52/gcgdata/geneseq/emb1/AA1980.DAT:\*  
2: /SID52/gcgdata/geneseq/emb1/AA1981.DAT:\*  
3: /SID52/gcgdata/geneseq/emb1/AA1982.DAT:\*  
4: /SID52/gcgdata/geneseq/emb1/AA1983.DAT:\*  
5: /SID52/gcgdata/geneseq/emb1/AA1984.DAT:\*  
6: /SID52/gcgdata/geneseq/emb1/AA1985.DAT:\*  
7: /SID52/gcgdata/geneseq/emb1/AA1986.DAT:\*  
8: /SID52/gcgdata/geneseq/emb1/AA1987.DAT:\*  
9: /SID52/gcgdata/geneseq/emb1/AA1988.DAT:\*  
10: /SID52/gcgdata/geneseq/emb1/AA1989.DAT:\*  
11: /SID52/gcgdata/geneseq/emb1/AA1990.DAT:\*  
12: /SID52/gcgdata/geneseq/emb1/AA1991.DAT:\*  
13: /SID52/gcgdata/geneseq/emb1/AA1992.DAT:\*  
14: /SID52/gcgdata/geneseq/emb1/AA1993.DAT:\*  
15: /SID52/gcgdata/geneseq/emb1/AA1994.DAT:\*  
16: /SID52/gcgdata/geneseq/emb1/AA1995.DAT:\*  
17: /SID52/gcgdata/geneseq/emb1/AA1996.DAT:\*  
18: /SID52/gcgdata/geneseq/emb1/AA1997.DAT:\*  
19: /SID52/gcgdata/geneseq/emb1/AA1998.DAT:\*  
20: /SID52/gcgdata/geneseq/emb1/AA1999.DAT:\*  
21: /SID52/gcgdata/geneseq/emb1/AA2000.DAT:\*  
22: /SID52/gcgdata/geneseq/emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	94.3	14	AAU76321	Synthetic Ghrelin
2	53.5	76.4	27	AAAB60514	Rat des-Gln14-ghre
3	53.5	76.4	27	AAAB60515	Human des-Gln14-gh
4	53.5	76.4	116	AAAB60516	Rat des-Gln14-ghre
5	53.5	76.4	116	AAAB60517	Human des-Gln14-gh
6	53	75.7	28	AAAG4993	Neurone denaturati
7	53	75.7	28	AAAB60508	Rat ghrelin, SEQ I
8	53	75.7	28	AAAB60509	Human ghrelin, SEQ
9	53	75.7	28	AAAB60530	Dog ghrelin-like G
10	53	75.7	28	AAE19032	Human ghrelin pept

11	53	75.7	28	23	AAE19041	Human ghrelin pept
12	53	75.7	90	23	ABP08975	Human ORFX protein
13	53	75.7	117	20	AAW87991	Protein designated
14	53	75.7	117	21	AAH87236	Human signal pepti
15	53	75.7	117	22	AAH38890	Human polypeptide
16	53	75.7	117	22	AAAB62649	Human zslg33 polyp
17	53	75.7	117	22	AAAB20101	Zslg33 protein, H
18	53	75.7	117	22	AAAB60510	Rat ghrelin prepro
19	53	75.7	117	22	AAAB60511	Human ghrelin pre
20	53	75.7	117	23	AAE23838	Human zslg33 proc
21	53	75.7	117	23	AAE15883	Human zslg33 proc
22	53	75.7	118	21	AAI66708	Membrane-bound pro
23	53	75.7	118	22	AAU12392	Human PRO1066 poly
24	53	75.7	118	22	AAAB65231	Human polypeptide
25	53	75.7	126	22	AAW40676	Porcine des-Gln14-
26	49.5	70.7	27	22	AAAB60519	Porcine des-Gln14-
27	49.5	70.7	117	22	AAAB60521	Porcine ghrelin, S
28	49	70.0	28	22	AAAB60518	Rat ghrelin-deriva
29	49	70.0	28	22	AAAB60560	Human ghrelin pept
30	49	70.0	28	23	AAE19021	Human ghrelin pept
31	49	70.0	28	23	AAE19027	Human ghrelin pept
32	49	70.0	28	23	AAE19028	Human ghrelin pept
33	49	70.0	28	23	AAE19029	Human ghrelin pept
34	49	70.0	28	23	AAE19030	Human ghrelin pept
35	49	70.0	28	23	AAE19031	Human ghrelin pept
36	49	70.0	28	23	AAE19033	Human ghrelin pept
37	49	70.0	28	23	AAE19034	Human ghrelin pept
38	49	70.0	28	23	AAE19035	Human ghrelin pept
39	49	70.0	28	23	AAE19036	Human ghrelin pept
40	49	70.0	28	23	AAE19037	Human ghrelin pept
41	49	70.0	28	23	AAE19038	Human ghrelin pept
42	49	70.0	28	23	AAE19039	Human ghrelin pept
43	49	70.0	28	23	AAE19040	Human ghrelin pept
44	49	70.0	118	22	AAAB60520	Porcine ghrelin, pr
45	44	62.9	23	22	AAAB60528	Rainbow trout 238a

ALIGNMENTS

RESULT 1	
AAU76321	AAU76321 standard; peptide; 14 AA.
XX	XX
AC	AAU76321;
XX	XX
DT	21-MAY-2002 (first entry)
XX	XX
DE	Synthetic Ghrelin variant #3.
XX	XX
KW	Ghrelin; antagonist; growth hormone release; octanoyl ester; tumour;
KW	acromegaly; osteopethtic.
XX	XX
OS	Synthetic.
XX	XX
FH	Key
FT	Modified-site 3 Location/Qualifiers
FT	/label= OTHER
FT	/note= "Other= Octanoyl Ser"
XX	XX
PN	WO200208250-A2.
XX	XX
PD	31-JAN-2002.
XX	XX
PF	10-JUL-2001; 2001WO-EP07929.
XX	XX
PR	24-JUL-2000; 2000US-220178P.
XX	XX
PA	(ZENT-) ZENTARIS AG.
PI	Deghenght R;
XX	XX
DR	WPI; 2002-206079/26.

XX New peptide which antagonises the effect of ghrelin when administered  
PT to a mammal -  
XX  
XX  
PS Claim 3; Page 6; 9pp; English.  
XX  
CC The invention relates to a novel peptide which antagonises the effect of  
CC ghrelin when administered to a mammal. The peptide is a synthetic  
CC analogue of ghrelin. Ghrelin is a 27-28 residue peptide isolated  
CC from distinctive cell types in the stomach of rats and humans and has an  
CC octanoyl ester attached to a serine residue. Ghrelin is a potent  
CC releaser of growth hormone. The peptides are useful for normalising  
CC elevated growth hormone levels in mammals such as those suffering  
CC from a tumour related to overproduction of growth hormone or acromegaly.  
CC The present sequence is a ghrelin antagonising peptide of the  
XX invention.  
XX  
SQ Sequence 14 AA;  
XX  
Query Match 94.3%; Score 66; DB 23; Length 14;  
Best Local Similarity 92.9%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GSSFLSPPEAKLQPR 14  
Db 1 GSKFLSPPEAKLQPR 14  
XX  
RESULT 2  
AAB60514  
ID AAB60514 standard; peptide; 27 AA.  
XX  
AC AAB60514;  
XX  
DT 24-APR-2001 (first entry)  
XX  
DE Rat des-Gln14-ghrelin, SEQ ID NO:10.  
XX  
KM Growth hormone secretagogue; GHS; ghrelin;  
KM calcium concentration elevation; infant growth disorder;  
KM growth hormone deficiency.  
XX  
OS Rattus norvegicus.  
XX  
PN WO200107475-A1.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-JP04907.  
XX  
PR 23-JUL-1999; 99JP-0210002.  
PR 29-NOV-1999; 99JP-0338841.  
PR 26-APR-2000; 2000JP-0126623.  
XX  
PA (KANG/) KANGAWA K.  
XX  
PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;  
XX  
DR WPI; 2001-159704/16.  
XX  
PT New peptide compounds which induce growth hormone secretion and  
PT elevate cell calcium concentrations, useful in treatment and diagnosis  
PT of infant growth disorders -  
XX  
PS Claim 3; Page 185; 210pp; Japanese.  
XX  
CC The invention relates to a novel peptide compound or its salt which  
CC induces the secretion of growth hormone and/or elevates calcium ion  
CC concentration in cells. The peptides are ghrelin homologues and are  
CC characterised in that at least one amino acid has been substituted by  
CC a modified amino acid and/or a non-amino acid compound. The invention  
CC also encompasses the unmodified peptides; the DNA encoding the peptides;  
CC vectors and host cells comprising such DNA; a method of producing the

CC peptides comprising recombinant production, optionally followed by  
CC chemical modification; an antibody specific for a peptide of the  
CC invention; and an assay and kit for detecting the peptides. The peptides  
CC of the invention are useful for treating and/or diagnosing diseases  
CC caused by a deficiency in growth hormone expression or activity. In  
CC particular, they are useful for promoting infant growth due to growth  
CC hormone deficiency. The compounds of the invention are safe with  
CC ghrelin-type growth hormone secretagogue (GHS) of the invention.  
XX  
SQ Sequence 27 AA;  
XX  
Query Match 76.4%; Score 53.5; DB 22; Length 27;  
Best Local Similarity 51.9%; Pred. No. 0.035;  
Matches 14; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
Qy 1 GSSFLSPPE-----AKLQPR 14  
Db 1 GSSFLSPPEHOKAKRKESKKPKLQPR 27  
XX  
RESULT 3  
AAB60515  
ID AAB60515 standard; peptide; 27 AA.  
XX  
AC AAB60515;  
XX  
DT 24-APR-2001 (first entry)  
XX  
DE Human des-Gln14-ghrelin, SEQ ID NO:11.  
XX  
KM Growth hormone secretagogue; GHS; ghrelin;  
KM calcium concentration elevation; infant growth disorder;  
KM growth hormone deficiency.  
XX  
OS Homo sapiens.  
XX  
PN WO200107475-A1.  
XX  
PD 01-FEB-2001.  
XX  
PF 24-JUL-2000; 2000WO-JP04907.  
XX  
PR 23-JUL-1999; 99JP-0210002.  
PR 29-NOV-1999; 99JP-0338841.  
PR 26-APR-2000; 2000JP-0126623.  
XX  
PA (KANG/) KANGAWA K.  
XX  
PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;  
XX  
DR WPI; 2001-159704/16.  
XX  
PT New peptide compounds which induce growth hormone secretion and  
PT elevate cell calcium concentrations, useful in treatment and diagnosis  
PT of infant growth disorders -  
XX  
PS Claim 3; Page 185; 210pp; Japanese.  
XX  
CC The invention relates to a novel peptide compound or its salt which  
CC induces the secretion of growth hormone and/or elevates calcium ion  
CC concentration in cells. The peptides are ghrelin homologues and are  
CC characterised in that at least one amino acid has been substituted by  
CC a modified amino acid and/or a non-amino acid compound. The invention  
CC also encompasses the unmodified peptides; the DNA encoding the peptides;  
CC peptides comprising recombinant production, optionally followed by  
CC chemical modification; an antibody specific for a peptide of the  
CC invention; and an assay and kit for detecting the peptides. The peptides  
CC of the invention are useful for treating and/or diagnosing diseases  
CC caused by a deficiency in growth hormone expression or activity. In  
CC particular, they are useful for promoting infant growth due to growth  
CC hormone deficiency. The compounds of the invention are safe with

CC no accompanying side effects. The present sequence represents a  
 CC ghrelin-type growth hormone secretagogue (GHS) of the invention.  
 XX  
 SQ Sequence 27 AA;

Query Match 76.4%; Score 53.5; DB 22; Length 27;  
 Best Local Similarity 51.9%; Pred. No. 0.035;  
 Matches 14; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

OY 1 GSSFLSPK-----AKLQPR 14  
 |||||  
 DB 1 GSSFLSPHQVRKSKKPPAKLQPR 27

RESULT 4  
 AAB60516  
 ID AAB60516 standard; Protein; 116 AA.

AC AAB60516;

DT 24-APR-2001 (first entry)

XX Rat des-Gln14-ghrelin preproprotein, SEQ ID NO:12.

KW Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;

KM calcium concentration elevation; infant growth disorder;

XX growth hormone deficiency.

OS Rattus norvegicus.

XX WO200107475-A1.

PD 01-FEB-2001.

PF 24-JUL-2000; 2000WO-JP04907.

PR 23-JUL-1999; 99JP-0210002.

PR 29-NOV-1999; 99JP-0338841.

PR 26-APR-2000; 2000JP-0126623.

XX (KANG/) KANGAWA K.

PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;

DR WPI; 2001-159704/16.

DR N-PSDB; AAF59646.

XX New peptide compounds which induce growth hormone secretion and

PT elevate cell calcium concentrations, useful in treatment and diagnosis

PT of infant growth disorders -

XX Claim 3; Page 186; 210pp; Japanese.

XX The invention relates to a novel peptide compound or its salt which

CC induces the secretion of growth hormone and/or elevates calcium ion

CC concentration in cells. The peptides are ghrelin homologues and are

CC characterised in that at least one amino acid has been substituted by

CC a modified amino acid and/or a non-amino acid compound. The invention

CC also encompasses the unmodified peptides; the DNA encoding the peptides;

CC vectors and host cells comprising such DNA; a method of producing the

CC peptides comprising recombinant production, optionally followed by

CC chemical modification; an antibody specific for the peptides. The peptides

CC of the invention are useful for detecting the peptides. The peptides

CC caused by a deficiency in growth hormone expression or activity. In

CC particular, they are useful for promoting infant growth due to growth

CC hormone deficiency. The compounds of the invention are safe with

CC no accompanying side effects. The present sequence represents a

CC ghrelin-type growth hormone secretagogue (GHS) precursor protein

CC of the invention.

XX Sequence 116 AA;

SQ

Query Match 76.4%; Score 53.5; DB 22; Length 116;  
 Best Local Similarity 51.9%; Pred. No. 0.17;  
 Matches 14; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

OY 1 GSSFLSPK-----AKLQPR 14  
 |||||  
 DB 24 GSSFLSPHQVRKSKKPPAKLQPR 50

RESULT 5  
 AAB60517  
 ID AAB60517 standard; Protein; 116 AA.

AC AAB60517;

DT 24-APR-2001 (first entry)

XX Human des-Gln14-ghrelin preproprotein, SEQ ID NO:13.

XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;

KM calcium concentration elevation; infant growth disorder;

XX growth hormone deficiency.

OS Homo sapiens.

XX WO200107475-A1.

PD 01-FEB-2001.

PF 24-JUL-2000; 2000WO-JP04907.

PR 23-JUL-1999; 99JP-0210002.

PR 29-NOV-1999; 99JP-0338841.

PR 26-APR-2000; 2000JP-0126623.

XX (KANG/) KANGAWA K.

PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;

DR WPI; 2001-159704/16.

DR N-PSDB; AAF59647.

XX New peptide compounds which induce growth hormone secretion and

PT elevate cell calcium concentrations, useful in treatment and diagnosis

PT of infant growth disorders -

XX Claim 3; Page 186-187; 210pp; Japanese.

XX The invention relates to a novel peptide compound or its salt which

CC induces the secretion of growth hormone and/or elevates calcium ion

CC concentration in cells. The peptides are ghrelin homologues and are

CC characterised in that at least one amino acid has been substituted by

CC a modified amino acid and/or a non-amino acid compound. The invention

CC also encompasses the unmodified peptides; the DNA encoding the peptides;

CC vectors and host cells comprising such DNA; a method of producing the

CC peptides comprising recombinant production, optionally followed by

CC chemical modification; an antibody specific for a peptide. The peptides

CC of the invention are useful for detecting the peptides. The peptides

CC caused by a deficiency in growth hormone expression or activity. In

CC particular, they are useful for promoting infant growth due to growth

CC hormone deficiency. The compounds of the invention are safe with

CC no accompanying side effects. The present sequence represents a

CC ghrelin-type growth hormone secretagogue (GHS) precursor protein

CC of the invention.

XX Sequence 116 AA;

SQ

Query Match 76.4%; Score 53.5; DB 22; Length 116;  
 Best Local Similarity 51.9%; Pred. No. 0.17;  
 Matches 14; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

OY 1 GSSFLSPK-----AKLQPR 14

Db 24 GSSFLSPFHQVRKESKKPKAKLQPR 50

RESULT 6  
AAG64943

ID AAG64943 standard; peptide; 28 AA.

AC AAG64943;

DT 19-OCT-2001 (first entry)

DE Neurone denaturation prevention method related peptide #5.

KM Neurone denaturation; neurone death; growth hormone liberation inhibitor;

KM cerebral infarction; oedema; Alzheimer's disease; Parkinson's disease;

KM Pick's disease; dementia; amyotrophic lateral sclerosis; cancer;

KM diabetic neuropathy; neuroprotective; antiinflammatory; nootropic;

OS cyostatic.

XX Unidentified.

XX Key

XX Modified-site

XX /label= OTHER

XX /note= "modified by O(C=O) (CH2) 6CH3"

XX WO200147558-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-JP09431.

XX 28-DEC-1999; 99JP-0375513.

XX (KAKE) KAKEN PHARM CO LTD.

XX Murata T, Ohyama T, Amakawa M, Fujita K, Ueo H;

XX WPI; 2001-536280/59.

XX Agents for treating diseases associated with denaturation or death of

XX neurons comprise growth hormone liberation inhibitor

XX Disclosure; Page 17; 50pp; Japanese.

XX The present invention provides agents for treating or preventing diseases

XX associated with denaturation or death of neurons, which comprise a

XX growth hormone liberation inhibitor. These can be used for treating or

XX preventing diseases associated with denaturation or death of neurons

XX including those due to cerebral ischaemic disorders such as cerebral

XX infarction or oedema. Other causes of denaturation or death of neurons

XX included Alzheimer's disease, Pick's disease, AIDS related dementia,

XX Parkinson's disease, amyotrophic lateral sclerosis, diabetic neuropathy

XX and anticancer treatments. The present sequence is a peptide described in

XX the exemplification of the invention.

XX Sequence 28 AA;

XX Query Match

XX Best Local Similarity 75.7%; Score 53; DB 22; Length 28;

XX Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

XX QY 1 GSSFLSPF-----AKLQPR 14

XX ID 1 GSSFLSPFHQVRKESKKPKAKLQPR 28

XX Db 1 GSSFLSPFHQVRKESKKPKAKLQPR 28

XX RESULT 7

XX AAB60508

XX ID AAB60508 standard; peptide; 28 AA.

XX XX AAB60508;

XX 24-APR-2001 (first entry)

DT Rat ghrelin, SEQ ID NO:2.

DE Growth hormone secretagogue; GHS; ghrelin;

KM calcium concentration elevation; infant growth disorder;

KM growth hormone deficiency.

XX Rattus norvegicus.

XX WO200107475-A1.

XX 01-FEB-2001.

XX 24-JUL-2000; 2000WO-JP04907.

XX 23-JUL-1999; 99JP-0210002.

XX 29-NOV-1999; 99JP-0338841.

XX 26-APR-2000; 2000JP-0126623.

XX (KANG/) KANGAWA K.

XX Kangawa K, Kojima M, Hosoda H, Matsu H, Minamitake Y;

XX WPI; 2001-159704/16.

XX Claim 2; Page 180; 210pp; Japanese.

XX The invention relates to a novel peptide compound or its salt which

XX induces the secretion of growth hormone and/or elevates calcium ion

XX concentration in cells. The peptides are ghrelin homologues and are

XX characterised in that at least one amino acid has been substituted by

XX a modified amino acid and/or a non-amino acid compound. The invention

XX also encompasses the unmodified peptides; the DNA encoding the peptides;

XX vectors and host cells comprising such DNA; a method of producing the

XX peptides comprising recombinant production, optionally followed by

XX chemical modification; an antibody specific for a peptide of the

XX invention; and an assay and kit for detecting the peptides. The peptides

XX of the invention are useful for treating and/or diagnosing diseases

XX caused by a deficiency in growth hormone expression or activity. In

XX particular, they are useful for promoting infant growth due to growth

XX hormone deficiency. The compounds of the invention are safe with

XX no accompanying side effects. The present sequence represents a

XX ghrelin-type growth hormone secretagogue (GHS) of the invention.

XX Sequence 28 AA;

XX Query Match

XX Best Local Similarity 75.7%; Score 53; DB 22; Length 28;

XX Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

XX QY 1 GSSFLSPF-----AKLQPR 14

XX ID 1 GSSFLSPFHQVRKESKKPKAKLQPR 28

XX Db 1 GSSFLSPFHQVRKESKKPKAKLQPR 28

XX RESULT 8

XX AAB60509

XX ID AAB60509 standard; peptide; 28 AA.

XX AC AAB60509;

XX 24-APR-2001 (first entry)

XX Human ghrelin, SEQ ID NO:3.

XX Growth hormone secretagogue; GHS; ghrelin;

XX calcium concentration elevation; infant growth disorder;

XX KW

KM growth hormone deficiency.  
 XX  
 PF Homo sapiens.  
 OS  
 XX MO200107475-A1.  
 PN  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 24-JUL-2000; 2000WO-JP04907.  
 XX  
 PR 23-JUL-1999; 99JP-0210002.  
 PR 29-NOV-1999; 99JP-0338841.  
 PR 26-APR-2000; 2000JP-0126623.  
 XX  
 PA (KANG/) KANGAWA K.  
 XX  
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;  
 DR WPI; 2001-159704/16.  
 XX  
 PT New peptide compounds which induce growth hormone secretion and  
 PT elevate cell calcium concentrations, useful in treatment and diagnosis  
 of infant growth disorders -  
 PS  
 XX Claim 3; Page 181; 210pp; Japanese.  
 XX  
 CC The invention relates to a novel peptide compound or its salt which  
 CC induces the secretion of growth hormone and/or elevates calcium ion  
 CC concentration in cells. The peptides are ghrelin homologues and are  
 CC characterised in that at least one amino acid has been substituted by  
 CC a modified amino acid and/or a non-amino acid compound. The invention  
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;  
 CC vectors and host cells comprising such DNA; a method of producing the  
 CC peptides comprising recombinant production, optionally followed by  
 CC chemical modification; an antibody specific for a peptide of the  
 CC invention; and an assay and kit for detecting the peptides. The peptides  
 CC of the invention are useful for treating and/or diagnosing diseases  
 CC caused by a deficiency in growth hormone expression or activity. In  
 CC particular, they are useful for promoting infant growth due to growth  
 CC hormone deficiency. The compounds of the invention are safe with  
 CC no accompanying side effects. The present sequence represents a  
 CC ghrelin-type growth hormone secretagogue (GHS) of the invention.  
 XX  
 SQ Sequence 28 AA;  
 XX  
 Query Match 75.7%; Score 53; DB 22; Length 28;  
 Best Local Similarity 50.0%; Pred. NO. 0.044;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 QY 1 GSSFLSP-----AKLQPR 14  
 DB 1 GSSFLSPHQKQRRKSKKPKAKLQPR 28  
 XX  
 RESULT 9  
 AAB60530  
 ID AAB60530 standard; peptide; 28 AA.  
 XX  
 AC AAB60530;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Dog ghrelin-like GH secretagogue peptide, SEQ ID NO:31.  
 XX  
 KM Growth hormone secretagogue; GHS; ghrelin;  
 KM calcium concentration elevation; infant growth disorder;  
 KM growth hormone deficiency.  
 XX  
 OS Canele familiaris.  
 XX  
 OS MO200107475-A1.  
 XX  
 PN  
 XX PD 01-FEB-2001.  
 XX

XX  
 PF 24-JUL-2000; 2000WO-JP04907.  
 XX  
 PR 23-JUL-1999; 99JP-0210002.  
 PR 29-NOV-1999; 99JP-0338841.  
 PR 26-APR-2000; 2000JP-0126623.  
 XX  
 PA (KANG/) KANGAWA K.  
 XX  
 PI Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;  
 DR WPI; 2001-159704/16.  
 XX  
 PT New peptide compounds which induce growth hormone secretion and  
 PT elevate cell calcium concentrations, useful in treatment and diagnosis  
 of infant growth disorders -  
 PS  
 XX Claim 4; Page 197; 210pp; Japanese.  
 XX  
 CC The invention relates to a novel peptide compound or its salt which  
 CC induces the secretion of growth hormone and/or elevates calcium ion  
 CC concentration in cells. The peptides are ghrelin homologues and are  
 CC characterised in that at least one amino acid has been substituted by  
 CC a modified amino acid and/or a non-amino acid compound. The invention  
 CC also encompasses the unmodified peptides; the DNA encoding the peptides;  
 CC vectors and host cells comprising such DNA; a method of producing the  
 CC peptides comprising recombinant production, optionally followed by  
 CC chemical modification; an antibody specific for a peptide of the  
 CC invention; and an assay and kit for detecting the peptides. The peptides  
 CC of the invention are useful for treating and/or diagnosing diseases  
 CC caused by a deficiency in growth hormone expression or activity. In  
 CC particular, they are useful for promoting infant growth due to growth  
 CC hormone deficiency. The compounds of the invention are safe with  
 CC no accompanying side effects. The present sequence represents a  
 CC ghrelin-type growth hormone secretagogue (GHS) of the invention.  
 XX  
 SQ Sequence 28 AA;  
 XX  
 Query Match 75.7%; Score 53; DB 22; Length 28;  
 Best Local Similarity 50.0%; Pred. NO. 0.044;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 QY 1 GSSFLSP-----AKLQPR 14  
 DB 1 GSSFLSPHQKQRRKSKKPKAKLQPR 28  
 XX  
 RESULT 10  
 AAE19032  
 ID AAE19032 standard; peptide; 28 AA.  
 XX  
 AC AAE19032;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX  
 DE Human ghrelin peptide analogue, compound 6.  
 XX  
 KM Human; ghrelin analogue; growth-hormone secretagogue; GHS receptor; AIDS;  
 KM acquired immune deficiency syndrome; weight gain; chemotherapy; dialysis;  
 KM growth hormone; muscle mass; bone density; sexual dysfunction; anorexia;  
 KM wasting; radiation therapy; obesity; diabetes; retinopathy; hypertension;  
 KM cardiovascular disorder; gall stone; osteoarthritis; cancer; cycostatic;  
 KM metabolic; immunomodulator; anti-HIV; anorectic; ophthalmological;  
 KM cardiant; litholytic; hepatotropic.  
 XX  
 OS Homo sapiens.  
 XX  
 OS MO200192292-A2.  
 XX  
 PN  
 XX PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US17026.  
 XX

```

PR 30-MAY-2000; 2000US-207920P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Bednarek M;
XX
XX WPI; 2002-195531/25.
XX
XX Truncated ghrelin analogs active at growth-hormone secretagogue
XX PT receptor useful for diagnosing or treating diseases such as anorexia,
XX PT bulimia, cancer, obesity, diabetes mellitus, hypertension,
XX PT osteoarthritis -
XX
XX Example 4; Page 34; 37pp; English.
XX
XX The present invention relates to a truncated ghrelin analogue or their
XX salt, active at growth-hormone secretagogue (GHS) receptor. Ghrelin
XX analogue is useful for screening a compound capable of binding to GHS
XX receptor and for stimulating growth hormone secretion. Ghrelin agonist
XX is utilised for treating a growth hormone deficient state, increasing
XX muscle mass and bone density, treating sexual dysfunction in males or
XX females, facilitating a weight gain, maintenance of weight, maintenance
XX of physical functioning, recovery of physical function, and/or appetite
XX increase, or appetite increase is particularly useful for a patient
XX having a disease or disorder, or under going a treatment, accompanied by
XX eight loss such as anorexia, bulimia, cancer cachexia, acquired
XX immune deficiency syndrome (AIDS), wasting, cachexia and wasting in frail
XX elderly and examples of treatments accompanied by weight loss include
XX chemotherapy, radiation therapy, temporary or permanent immobilisation
XX and dialysis; and ghrelin antagonist is utilised to facilitate weight
XX loss, appetite decrease, weight maintenance, treat obesity, diabetes and
XX complications of diabetes including retinopathy, and/or cardiovascular
XX disorders, where excessive weight is a contributing factor to different
XX diseases including hypertension, diabetes, dyslipidemias, cardiovascular
XX disease, gall stones, osteoarthritis and certain forms of cancers, and
XX bringing about a weight loss can be used for e.g. to reduce the
XX likelihood of such diseases and for treating such diseases. Ghrelin
XX analogue induces growth hormone release from primary-culture pituitary
XX cells in a dose-dependent manner without stimulating the release of other
XX pituitary hormones. Unlike longer length ghrelin, ghrelin analogue can be
XX synthesised easily and has increased solubility in physiological buffers.
XX The present sequence is human ghrelin peptide analogue.
XX
XX Sequence 28 AA;
XX
XX Query Match 75.7%; Score 53; DB 23; Length 28;
XX Best Local Similarity 50.0%; Pred. NO. 0.044;
XX Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
XX
XX 1 GSSFLSPF-----AKIQPR 14
XX ||||| |||||
XX 1 GSSFLSPHQRVQQRKXKPKAQPR 28
XX
XX RESULT 11
XX ID AAE19041 standard; peptide: 28 AA.
XX AC AAE19041;
XX XX
XX DT 21-MAY-2002 (first entry)
XX
XX DE Human ghrelin peptide analogue, compound 17.
XX
XX Human; ghrelin analogue; growth-hormone secretagogue; GHS receptor; AIDS;
XX acquired immune deficiency syndrome; weight gain; chemotherapy; dialysis;
XX growth hormone; muscle mass; bone density; sexual dysfunction; anorexia;
XX wasting; radiation therapy; obesity; diabetes; retinopathy; hypertension;
XX cardiovascular disorder; gall stone; osteoarthritis; cancer; cytostatic;
XX metabolic; immunomodulator; anti-HIV; anorectic; ophthalmological;
XX cardiac; litholytic; hepatotropic.
XX
XX Homo sapiens.
XX OS

```

```

XX
XX Key Location/Qualifiers
XX FT Modified-site 3
XX FT /note= "Ser(CO-(CH2)6-CH3)"
XX
XX WO200192292-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US17026.
XX
XX 30-MAY-2000; 2000US-207920P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Bednarek M;
XX
XX WPI; 2002-195531/25.
XX
XX Truncated ghrelin analogs active at growth-hormone secretagogue
XX PT receptor useful for diagnosing or treating diseases such as anorexia,
XX PT bulimia, cancer, obesity, diabetes mellitus, hypertension,
XX PT osteoarthritis -
XX
XX Example 4; Page 23; 37pp; English.
XX
XX The present invention relates to a truncated ghrelin analogue or their
XX salt, active at growth-hormone secretagogue (GHS) receptor. Ghrelin
XX analogue is useful for screening a compound capable of binding to GHS
XX receptor and for stimulating growth hormone secretion. Ghrelin agonist
XX is utilised for treating a growth hormone deficient state, increasing
XX muscle mass and bone density, treating sexual dysfunction in males or
XX females, facilitating a weight gain, maintenance of weight, maintenance
XX of physical functioning, recovery of physical function, and/or appetite
XX increase, or appetite increase is particularly useful for a patient
XX having a disease or disorder, or under going a treatment, accompanied by
XX eight loss such as anorexia, bulimia, cancer cachexia, acquired
XX immune deficiency syndrome (AIDS), wasting, cachexia and wasting in frail
XX elderly and examples of treatments accompanied by weight loss include
XX chemotherapy, radiation therapy, temporary or permanent immobilisation
XX and dialysis; and ghrelin antagonist is utilised to facilitate weight
XX loss, appetite decrease, weight maintenance, treat obesity, diabetes and
XX complications of diabetes including retinopathy, and/or cardiovascular
XX disorders, where excessive weight is a contributing factor to different
XX diseases including hypertension, diabetes, dyslipidemias, cardiovascular
XX disease, gall stones, osteoarthritis and certain forms of cancers, and
XX bringing about a weight loss can be used for e.g. to reduce the
XX likelihood of such diseases and for treating such diseases. Ghrelin
XX analogue induces growth hormone release from primary-culture pituitary
XX cells in a dose-dependent manner without stimulating the release of other
XX pituitary hormones. Unlike longer length ghrelin, ghrelin analogue can be
XX synthesised easily and has increased solubility in physiological buffers.
XX The present sequence is human ghrelin peptide analogue.
XX
XX Sequence 28 AA;
XX
XX Query Match 75.7%; Score 53; DB 23; Length 28;
XX Best Local Similarity 50.0%; Pred. NO. 0.044;
XX Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
XX
XX 1 GSSFLSPF-----AKIQPR 14
XX ||||| |||||
XX 1 GSSFLSPHQRVQQRKXKPKAQPR 28
XX
XX RESULT 12
XX ID ABP08975 standard; Protein; 90 AA.
XX AC ABP08975;
XX XX
XX DT 24-JUN-2002 (first entry)
XX

```

DE Human ORFX protein sequence SEQ ID NO:17932.  
XX  
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
KM hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
KM degenerative disorder; osteoarthritis; neurodegenerative disorder;  
KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
KM hypertension; hypothyroidism; cholesterol ester storage disease;  
KM immune deficiency; immune disorder; infectious disease;  
KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
KM myasthenia gravis.  
XX  
XX Homo sapiens.  
OS  
XX WO200192523-A2.  
PN  
XX 06-DEC-2001.  
PD  
XX  
XX 29-MAY-2001; 2001MO-US10836.  
PF  
XX  
XX 30-MAY-2000; 2000US-206132P.  
PR  
XX 29-AUG-2000; 2000US-228716P.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shimketa RA, Leach MD;  
PI  
XX WPI; 2002-106308/14.  
DR  
XX N-PSDB; ABN24727.  
DR  
XX  
XX Novel human polypeptides and polynucleotides useful for diagnosing,  
PT preventing and treating cardiovascular disease, neurodegenerative,  
PT hyperproliferative disorders and autoimmune disorders -  
XX  
XX  
XX Disclosure; SEQ ID 17932; 1037pp; English.  
XX  
XX The present invention describes substantially purified human proteins  
CC (referred to as open reading frame, ORPX, where X is 1-11491 (see Table 1  
CC in the specification)). ABN15762 to ABN27252 encode the human ORFX  
CC protein given in ABP00010 to ABP11500. ORFX proteins are useful for  
CC treating or preventing a pathology associated with an ORFX-associated  
CC disorder in humans, and in the manufacture of a medicament for treating a  
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
CC sequences can be used in gene therapy. ORFX sequences can be used in the  
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,  
CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
CC storage disease, various immune deficiencies and disorders, infectious  
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
CC bone degenerative disorders, or periodontal disease, and for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues and conditions resulting from  
CC systemic cytokine damage.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIFO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX  
SQ Sequence 90 AA;  
Query Match 75.7%; Score 53; DB 23; Length 90;  
Best Local Similarity 50.0%; Pred. No. 0.15;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
QY 1 GSSFLSPSE-----AKLQPR 14  
|||  
Db 24 GSSFLSPSEHQAKQQRKSKKPAKLQPR 51  
|||  
RESULT 13

AAW87991  
ID AAW87991 standard; Protein; 117 AA.  
XX  
XX AAW87991;  
AC  
XX 07-APR-1999 (first entry)  
DT  
XX  
XX Protein designated zsig33.  
DE  
XX  
XX Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;  
KM nutrient absorption regulation; obesity; metabolic disorder.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1..23  
FT Peptide /note="signal peptide"  
FT Protein /note="mature protein"  
FT  
XX  
XX MO9842840-A1.  
XX  
XX 01-OCT-1998.  
PD  
XX  
XX 23-MAR-1998; 98WO-US05620.  
PF  
XX  
XX 24-MAR-1997; 97US-0822897.  
PR  
XX 24-MAR-1997; 97US-0041102.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
PA  
XX  
XX Delsner TA, Shepard PO;  
PI  
XX  
XX WPI; 1999-070071/06.  
DR  
XX N-PSDB; AAX04550.  
DR  
XX  
XX Human polypeptide having homology to motilin, zsig33 - useful e.g.  
PT to treat gastrointestinal motility disorders, obesity etc. and to  
PT identify antagonists to treat gastrointestinal hypermotility  
XX  
XX Claim 13; Page 55-56; 69pp; English.  
XX  
XX The present sequence represents a protein designated Zsig33. The nucleic  
CC acids are strongly expressed in stomach tissue. The polypeptide (or  
CC allelic variants/orthologs) can be used to stimulate gastric motility,  
CC measured as increased transit time or gastric emptying of an ingested  
CC substance in mammals. The products are used to treat disorders associated  
CC with gastrointestinal cell contractility, secretion of digestive  
CC enzymes/acids, gastrointestinal motility, recruitment of digestive  
CC enzymes, gastrointestinal inflammation, reflux disease and nutrient  
CC absorption regulation. Zsig33 polypeptides may also be important  
CC neurologically, since the family of gut-brain peptides to which the  
CC homologous protein motilin belongs has been associated with neurological  
CC and CNS functions. They may therefore be used e.g. to regulate satiety  
CC or treat obesity and other metabolic disorders where neurological  
CC feedback modulates nutritional absorption. They are useful to identify  
CC zsig33 agonists, antagonists and ligands and to produce antibodies.  
XX  
XX  
SQ Sequence 117 AA;  
Query Match 75.7%; Score 53; DB 20; Length 117;  
Best Local Similarity 50.0%; Pred. No. 0.2;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
QY 1 GSSFLSPSE-----AKLQPR 14  
|||  
Db 24 GSSFLSPSEHQRVQQRKSKKPAKLQPR 51  
|||  
RESULT 14  
AAI87236  
ID AAY87236 standard; Protein; 117 AA.  
XX

AC AAY87236;  
 XX  
 DT 11-MAY-2000 (first entry)  
 XX  
 DE Human signal peptide containing protein HSPB-13 SEQ ID NO:13.  
 XX  
 KW Human; signal peptide-containing protein; HSPB; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;  
 KW antiaesthetic; gene therapy; cell proliferation; neurological disorder;  
 KW reproductive disorder; developmental disorder; arteriosclerosis;  
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;  
 KW muscular dystrophy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200000610-A2.  
 XX  
 PD 06-JAN-2000.  
 XX  
 PF 25-JUN-1999; 99WO-US14484.  
 XX  
 PR 26-JUN-1999; 98US-0090762.  
 PR 31-OCT-1998; 98US-0094983.  
 PR 01-OCT-1998; 98US-0102686.  
 PR 11-DEC-1999; 98US-0112129.  
 XX  
 PA (INCYTE) INCYTE PHARM INC.  
 XX  
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
 PI Akeblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
 PI Bandman O;  
 XX  
 DR WPI; 2000-160673/14.  
 XX  
 PT N-PSDB; AAY98121.  
 XX  
 PT New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and  
 PT cardiovascular disease  
 XX  
 PS Claim 1; Page 168-169; 327pp; English.  
 XX  
 CC AAY98109 to AAY98242 encode AAY87224 to AAY87357 which represent the  
 CC human signal peptide-containing proteins HSPB-1 to HSPB-134. HSPBs have  
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,  
 CC neuroprotective, cardiovascular and antiaesthetic activities, and can  
 CC be used in gene therapy. HSPBs can be used to treat or prevent disorders  
 CC associated with decreased activity or function of HSPB. Antagonists of  
 CC HSPB are used to treat or prevent disorders associated with increased  
 CC activity or function of HSPB. Such diseases include cell proliferation  
 CC (including cancer), inflammation, cardiovascular, neurological,  
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
 CC asthma, Crohn's disease, microbial or other infections, congestive or  
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPB  
 CC nucleic acids can be used for the recombinant production of HSPB, for  
 CC detecting HSPB in standard hybridisation and amplification assays (for  
 CC diagnosis and monitoring), in gene therapy, as antisense,  
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
 CC or genetic variations, and for chromosomal mapping. HSPB are also used to  
 CC raise specific antibodies (Ab) and to screen for agonists and  
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
 CC monitor, HSPB-related diseases (in usual immunoassays), as therapeutic  
 CC antagonists, in competitive drug screens, and for purification of HSPB  
 CC from natural sources.  
 XX  
 SQ Sequence 117 AA;

Query Match 75.7%; Score 53; DB 21; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.2;

Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 QY 1 GSSFLSP-----AKLQPR 14  
 |||||  
 DB 24 GSSFLSPHQRYQGRKESKPPAKLQPR 51  
 |||||  
 RESULT 15  
 AAM38890  
 ID AAM38890 standard; Protein, 117 AA.  
 XX  
 AC AAM38890;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 2035.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Dymnanc RT;  
 XX  
 DR WPI; 2001-442253/47.  
 XX  
 PT N-PSDB; AAI58046.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Example 3; SEQ ID NO 2035; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 CC the encoded polypeptides (AAM38642-AAI42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localized neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX  
 SQ Sequence 117 AA;



Query Match 75.78; Score 53; DB 22; Length 117;  
Best Local Similarity 50.08; Pred. No. 0.2;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
Oy 1 GSFSLSPK-----AKLQPR 14  
Db 24 GSFSLSPKRNQVRQQRKSKPPAKLQPR 51

Search completed: January 29, 2003, 13:22:43  
Job time : 36 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using SW model

Run on: January 29, 2003, 13:22:47 ; Search time 14 Seconds  
(without alignments)  
29.423 Million cell updates/sec

Title: MAYES-902-SEQ1  
Perfect score: 70  
Sequence: 1 gsaflpeaklqpr 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued\_Patents\_AA.\*  
2: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backflrst.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	75.7	117	4	US-09-046-479-2
2	53	75.7	117	4	US-08-822-897C-2
3	53	75.7	117	4	US-09-608-810A-4
4	40	57.1	11	4	US-09-608-810A-2
5	37	52.9	417	1	US-07-649-591B-7
6	37	52.9	417	1	US-08-237-540-7
7	37	52.9	417	1	US-08-430-787A-7
8	37	52.9	778	4	US-09-460-145-2
9	37	52.9	797	4	US-09-460-145-4
10	37	52.9	913	3	US-08-827-208-3
11	37	52.9	913	4	US-09-500-358-3
12	37	52.9	913	4	US-09-498-809-3
13	36	51.4	57	2	US-08-598-873-36
14	36	51.4	57	2	US-08-605-430-36
15	35	50.0	263	5	PCT-US91-08177-13
16	35	50.0	894	4	US-08-599-455B-2
17	35	50.0	894	4	US-09-069-781B-2
18	35	50.0	894	4	US-08-618-957A-12
19	35	50.0	894	4	US-09-137-132-2
20	35	50.0	894	4	US-08-864-564A-2
21	35	50.0	894	4	US-09-094-410-2
22	35	50.0	895	4	US-08-827-962-19
23	35	50.0	895	4	US-08-827-962-21
24	35	50.0	896	2	US-08-640-389A-12
25	35	50.0	905	4	US-09-369-364A-9
26	35	50.0	940	2	US-08-938-365-4
27	35	50.0	941	1	US-08-343-760A-2

28	35	50.0	1162	2	US-08-599-455B-43	Sequence 43, Appl
29	35	50.0	1162	4	US-08-827-962-15	Sequence 15, Appl
30	35	50.0	1162	4	US-08-827-962-20	Sequence 20, Appl
31	35	50.0	1162	4	US-08-803-346-1	Sequence 1, Appl
32	35	50.0	1162	4	US-09-069-781B-43	Sequence 43, Appl
33	35	50.0	1162	4	US-09-137-132-43	Sequence 43, Appl
34	35	50.0	1162	4	US-08-864-564A-43	Sequence 43, Appl
35	35	50.0	1162	4	US-09-094-410-43	Sequence 43, Appl
36	35	50.0	2353	4	US-08-984-709A-50	Sequence 50, Appl
37	35	50.0	2409	6	5180808-2	Patent No. 5180808
38	34	48.6	166	2	US-08-627-610-12	Sequence 12, Appl
39	34	48.6	166	3	US-08-384-106A-2	Sequence 2, Appl
40	34	48.6	166	3	US-08-384-106A-17	Sequence 17, Appl
41	34	48.6	166	3	US-08-384-106A-22	Sequence 22, Appl
42	34	48.6	166	3	US-09-240-906-4	Sequence 4, Appl
43	34	48.6	166	5	PCT-US96-01643-2	Sequence 2, Appl
44	34	48.6	166	5	PCT-US96-05252-4	Sequence 4, Appl
45	34	48.6	310	4	US-09-632-947B-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1

US-09-046-479-2

Sequence 2, Application US/09046479

Patent No. 6291653

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

APPLICANT: Deisher, Theresa A.

TITLE OF INVENTION: MOTILIN HOMOLOGS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/046,479

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAMES: Sawislak, Deborah A.

REGISTRATION NUMBER: 37,438

REFERENCE/DOCKET NUMBER: 97-04

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6672

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-046-479-2

Query Match

Best Local Similarity 75.7%; Score 53; DB 4; Length 117;

Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 GSSFLSPE-----AKLOPR 14  
 Db 24 GSSFLSPHQRVQQRKSKKPPAKLOPR 51

RESULT 2  
 US-08-822-897C-2  
 ; Sequence 2, Application US/08822897C  
 ; Patent No. 6380158  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Deisher, Theresa A.  
 ; TITLE OF INVENTION: MOTILIN HOMOLOGS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ZymoGenetics, Inc.  
 ; STREET: 1201 Eastlake Avenue East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/822,897C  
 ; FILING DATE:  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sawislak, Deborah A  
 ; REGISTRATION NUMBER: 37,438  
 ; REFERENCE/DOCKET NUMBER: 97-04  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6672  
 ; TELEFAX: 206-442-6678  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 117 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-08-822-897C-2

Query Match

Best Local Similarity 75.7%; Score 53; DB 4; Length 117;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 GSSFLSPE-----AKLOPR 14  
 Db 24 GSSFLSPHQRVQQRKSKKPPAKLOPR 51

RESULT 3  
 US-09-608-810A-4  
 ; Sequence 4, Application US/09608810A  
 ; Patent No. 6420521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Jaepers, Stephen R.  
 ; APPLICANT: Deisher, Theresa A.  
 ; APPLICANT: Bishop, Paul D.  
 ; TITLE OF INVENTION: SGIP PEPTIDES  
 ; FILE REFERENCE: 99-51  
 ; CURRENT APPLICATION NUMBER: US/09/608,810A  
 ; CURRENT FILING DATE: 2000-06-30

;; PRIOR APPLICATION NUMBER: 60/141,592  
 ;; PRIOR FILING DATE: 1999-06-30  
 ;; NUMBER OF SEQ ID NOS: 7  
 ;; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ;; SEQ ID NO 4  
 ;; LENGTH: 117  
 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 ;; FEATURE:  
 ;; NAME/KEY: SIGNAL  
 ;; LOCATION: (1)...(23)  
 ; US-09-608-810A-4

Query Match  
 Best Local Similarity 75.7%; Score 53; DB 4; Length 117;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 GSSFLSPE-----AKLOPR 14  
 Db 24 GSSFLSPHQRVQQRKSKKPPAKLOPR 51

RESULT 4  
 US-09-608-810A-2  
 ; Sequence 2, Application US/09608810A  
 ; Patent No. 6420521  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Jaepers, Stephen R.  
 ; APPLICANT: Deisher, Theresa A.  
 ; APPLICANT: Bishop, Paul D.  
 ; TITLE OF INVENTION: SGIP PEPTIDES  
 ; FILE REFERENCE: 99-51  
 ; CURRENT APPLICATION NUMBER: US/09/608,810A  
 ; CURRENT FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: 60/141,592  
 ; PRIOR FILING DATE: 1999-06-30  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-608-810A-2

Query Match  
 Best Local Similarity 57.1%; Score 40; DB 4; Length 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSFLSPE 8  
 Db 1 GSSFLSPE 8

RESULT 5  
 US-07-649-591B-7  
 ; Sequence 7, Application US/07649591B  
 ; Patent No. 5206161  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dennis Drayna and Daniel Eaton  
 ; TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/649,591B
; FILING DATE: 19910201
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haasek, Janet E.
; REGISTRATION NUMBER: 28,616
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-649-591B-7

Query Match          52.9%; Score 37; DB 1; Length 417;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 SSFLSPKALQIP 13
Db      385 SGFLPSRIKP 396

-RESULT 6
US-08-277-540-7
; Sequence 7, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Baton, Dan L.
; TITLE OF INVENTION: NO. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Haasek, Janet E.
; REGISTRATION NUMBER: 28,616
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
```

```

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-277-540-7

Query Match          52.9%; Score 37; DB 1; Length 417;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 SSFLSPKALQIP 13
Db      385 SGFLPSRIKP 396

-RESULT 7
US-08-430-787A-7
; Sequence 7, Application US/08430787A
; Patent No. 5593674
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Baton, Dan L.
; TITLE OF INVENTION: NO. 5593674el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,787A
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,540
; FILING DATE: 19-JUL-1994
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Haasek, Janet E.
; REGISTRATION NUMBER: 28,616
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-430-787A-7

Query Match          52.9%; Score 37; DB 1; Length 417;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 SSFLSPKALQIP 13
Db      385 SGFLPSRIKP 396
```

```

RESULT 8
US-09-460-145-2
; Sequence 2, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
; APPLICANT: Kitz, Ron
; APPLICANT: Song, Chuanzheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,145
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/788,975
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 778 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-460-145-2

Query Match      52.9%; Score 37; DB 4; Length 778;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14
Db 668 SPEEQLOPR 676

RESULT 9
US-09-460-145-4
; Sequence 4, Application US/09460145
; Patent No. 6287838
; GENERAL INFORMATION:
; APPLICANT: Kitz, Ron
; APPLICANT: Song, Chuanzheng
; TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,145
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/788,975
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-460-145-4

```

```

Query Match      52.9%; Score 37; DB 4; Length 797;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14
Db 687 SPEEQLOPR 695

```

```

RESULT 10
US-08-827-208-3
; Sequence 3, Application US/08827208
; Patent No. 6025178
; GENERAL INFORMATION:
; APPLICANT: Chion, Xue-Chiou C.
; APPLICANT: Kramet, Ruth M.
; APPLICANT: Pickard, Richard T.
; APPLICANT: Sharp, John D.
; APPLICANT: Striffler, Beth A.
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
; NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,208
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/014,608
; FILING DATE: 29-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,264
; FILING DATE: 19-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808

```

REFERENCE/DOCKET NUMBER: X-10610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 913 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-827-208-3

Query Match 52.9%; Score 37; DB 3; Length 913;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
DB 803 SPEQLOPR 811

## RESULT 11

US-09-500-358-3  
Sequence 3, Application US/09500358  
Patent No. 6197569  
GENERAL INFORMATION:  
APPLICANT: Chlou, Xue-Chiou C.  
APPLICANT: Kramer, Ruth M.  
APPLICANT: Pickard, Richard T.  
APPLICANT: Sharp, John D.  
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED  
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,358  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,208  
FILING DATE: 28-MAR-1997  
APPLICATION NUMBER: US 60/014,608  
FILING DATE: 29-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/041,264  
FILING DATE: 19-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-10610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 913 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-500-358-3

Query Match 52.9%; Score 37; DB 4; Length 913;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
DB 803 SPEQLOPR 811

## RESULT 12

US-09-498-809-3  
Sequence 3, Application US/09498809  
Patent No. 6242206  
GENERAL INFORMATION:  
APPLICANT: Chlou, Xue-Chiou C.  
APPLICANT: Kramer, Ruth M.  
APPLICANT: Pickard, Richard T.  
APPLICANT: Sharp, John D.  
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED  
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,809  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/827,208  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/041,264  
FILING DATE: 19-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-10610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 913 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-498-809-3

Query Match 52.9%; Score 37; DB 4; Length 913;  
Best Local Similarity 77.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
DB 803 SPEQLOPR 811

RESULT 13  
US-08-598-873-36  
Sequence 36, Application US/08598873  
Patent No. 5928884  
GENERAL INFORMATION:

```

; APPLICANT: Croce, Carlo M.
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,873
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-598-873-36

Query Match      51.4%; Score 36; DB 2; Length 57;
Best Local Similarity 58.3%; Pred. No. 8.8;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SSFISPEAKLOP 13
Db 3 SFISPCXLOP 14

RESULT 14
; US-08-605-430-36
; Sequence 36, Application US/08605430
; Patent No. 6242212
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,430
; FILING DATE: 22-FEB-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-605-430-36

Query Match      51.4%; Score 36; DB 4; Length 57;
Best Local Similarity 58.3%; Pred. No. 8.8;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SSFISPEAKLOP 13
Db 3 SFISPCXLOP 14

RESULT 15
; PCT-US91-08177-13
; Sequence 13, Application PC/TUS9108177
; GENERAL INFORMATION:
; APPLICANT: Samal, Siba K
; TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08177
; FILING DATE: 19911104
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/608,937
; FILING DATE: 05-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hiehet, David W
; REGISTRATION NUMBER: 30,265
; REFERENCE/DOCKET NUMBER: 20509-96711
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4854
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-08177-13

Query Match      50.0%; Score 35; DB 5; Length 263;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 SPEAKLOP 14
Db 224 SPEAKLOP 232

```



Search completed: January 29, 2003, 13:24:20  
Job time : 15 secs

---

**THIS PAGE BLANK (USPTO)**

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: January 29, 2003, 13:21:32 ; Search time 15 Seconds  
(without alignments)  
89.725 Million cell updates/sec

Title: MAYES-902-SEQ1  
Perfect score: 70  
Sequence: 1 gssflspeak1qpr 14

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	75.7	117	1 A59316	ghrelin precursor
2	53	75.7	117	1 B59316	ghrelin precursor
3	43	61.4	248	2 PQ0769	glycoprotein G - b
4	43	61.4	250	2 PQ0768	glycoprotein G - b
5	42	60.0	104	2 S73927	ribosomal protein
6	42	60.0	105	2 B64210	ribosomal protein
7	41	58.6	164	2 T23249	hypothetical prote
8	41	58.6	283	2 S34851	hypothetical 31.9K
9	40	57.1	208	2 H87334	conserved hypothet
10	40	57.1	308	2 H87306	glycosyl transfera
11	40	57.1	343	2 AB1086	ATP synthase delta
12	40	57.1	343	2 AH1449	weakly ATP synhas
13	40	57.1	709	1 TMBYSS	transcription fact
14	39	55.7	257	1 MGNZBR	major surface glyc
15	39	55.7	371	2 T49100	hypothetical prote
16	39	55.7	473	2 T46999	hypothetical prote
17	39	55.7	473	2 AC0239	probable GntR-fam1
18	39	55.7	558	1 A39633	transcription fact
19	39	55.7	742	2 S55098	probable membrane
20	38	55.0	681	2 T01469	hypothetical prote
21	38	54.3	108	2 T04117	SCC18 protein homo
22	38	54.3	226	2 G75342	hypothetical prote
23	38	54.3	459	2 B89927	hypothetical prote
24	38	54.3	770	2 H84463	hypothetical prote
25	38	54.3	993	2 A46415	basophilic - human
26	38	54.3	1137	2 T19414	hypothetical prote
27	38	54.3	1172	2 T00065	CS6 structural sub
28	37	52.9	154	2 T60266	ctd-p-rlha, A-D-glc
29	37	52.9	293	2 G98163	

30	37	52.9	293	2 AB3124	glycosyltransferas
31	37	52.9	304	2 T46003	hypothetical prote
32	37	52.9	309	2 A38395	mast cell carboxyp
33	37	52.9	321	2 A95182	hypothetical prote
34	37	52.9	322	2 D98049	thioester-dioluf
35	37	52.9	357	2 AF0243	probable exported
36	37	52.9	391	2 T30149	hypothetical prote
37	37	52.9	417	1 A34487	carboxypeptidase A
38	37	52.9	426	2 T00848	probable serine/th
39	37	52.9	426	2 T52285	serine/threonine-s
40	37	52.9	577	2 G83599	probable gamma-glu
41	37	52.9	603	2 A10741	phosphogluconate d
42	37	52.9	739	2 T02996	N-ethylmaleimide s
43	37	52.9	982	2 A53253	microtubule-associ
44	37	52.9	1152	2 A33183	microtubule-associ
45	37	52.9	1495	2 S27001	alpha-2-macroglobu

## ALIGNMENTS

RESULT 1  
A59316  
ghrelin precursor - human  
N:Alternate names: preproghrelin  
C:Species: Homo sapiens (man)  
C>Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 21-Jul-2000  
C/Accession: A59316  
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.  
N:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.  
A:Reference number: A59316; UID:20067959; PMID:10604470  
A/Accession: A59316  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-117 <KOJ>  
A/Cross-references: GB:AB029434; NID:G6691571; PIDN:BA089371.1; PID:G6691572  
A/Experimental source: tissue stomach endocrine cells  
A/Note: submitted to GenBank, June 1999  
C/Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (grow.  
C/Superfamily: motilin  
C/Keywords: hormone; lipoprotein; stomach  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-51/Product: ghrelin #status predicted <MAT>  
F:52-117/Domain: carboxyl-terminal propetide #status predicted <CNP>  
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match  
Best Local Similarity 50.0%; Pred. No. 0.027;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 GSSFLSPR-----AKLQPR 14  
DB 24 GSSFLSPRHQVQORRKKSKPKAPKQPR 51

RESULT 2  
B59316  
ghrelin precursor - rat  
N:Alternate names: preproghrelin  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 21-Jul-2000  
C/Accession: B59316  
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.  
N:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.  
A:Reference number: A59316; UID:20067959; PMID:10604470  
A/Accession: B59316  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA; protein  
A/Residues: 1-117 <KOJ>  
A/Cross-references: GB:AB029433; NID:G6691569; PIDN:BA089370.1; PID:G6691570  
A/Experimental source: strain SD; tissue stomach endocrine cells

A>Note: submitted to GenBank, June 1999  
 C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth)  
 C:Superfamily: molitin  
 C:Keywords: hormone; lipoprotein; stomach  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-51/Product: ghrelin #status predicted <MAT>  
 F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
 F:26/Binding site: octanote (Ser) (covalent) #status experimental

Query Match 75.7%; Score 53; DB 1; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.027;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

Oy 1 GSSFLSP-----AKLOPR 14  
 Db 24 GSSFLSPHQKQQRKSKPKAKLOPR 51

RESULT 3  
 P00769  
 glycoprotein G - bovine respiratory syncytial virus (isolate VC464) (fragment)  
 C:Species: bovine respiratory syncytial virus  
 C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
 C:Accession: P00769  
 R:Mailpeddi, S.K.; Samal, S.K.  
 J. Gen. Virol. 74, 2001-2004, 1993  
 A:Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial v  
 A:Reference number: J02284; MUID:93389461; PMID:8376974  
 A:Accession: P00769  
 A:Molecule type: mRNA  
 A:Residues: 1-248 <MAL>  
 A:Experimental source: isolate VC464  
 A>Note: the authors translated the codon ACC for residue 85 as His and ATC for residue 2  
 C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-29/Domain: intracellular #status predicted <INT>  
 F:30-57/Domain: transmembrane #status predicted <TM>  
 F:58-248/Domain: extracellular #status predicted <EXT>  
 F:76,154,224,242/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 43; DB 2; Length 248;  
 Best Local Similarity 88.9%; Pred. No. 4;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 SPEAKLOPR 14  
 Db 215 SPEAKLOPR 223

RESULT 4  
 P00768  
 glycoprotein G - bovine respiratory syncytial virus (isolate FS-1) (fragment)  
 C:Species: bovine respiratory syncytial virus  
 C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 07-May-1999  
 C:Accession: P00768  
 R:Mailpeddi, S.K.; Samal, S.K.  
 J. Gen. Virol. 74, 2001-2004, 1993  
 A:Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial v  
 A:Reference number: J02284; MUID:93389461; PMID:8376974  
 A:Accession: P00768  
 A:Molecule type: mRNA  
 A:Residues: 1-250 <MAL>  
 C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-31/Domain: intracellular #status predicted <INT>  
 F:32-59/Domain: transmembrane #status predicted <TM>  
 F:60-250/Domain: extracellular #status predicted <EXT>  
 F:78,156,226,241,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 43; DB 2; Length 250;  
 Best Local Similarity 88.9%; Pred. No. 4.1;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 SPEAKLOPR 14  
 Db 217 SPEAKLOPR 225

RESULT 5  
 S73927  
 ribosomal protein S18 - Mycoplasma pneumoniae (strain ATCC 29342)  
 N:Alternate names: hypothetical protein G07\_orf104b  
 C:Species: Mycoplasma pneumoniae  
 A:Variety: ATCC 29342  
 C:Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
 C:Accession: S73927  
 R:Himmelreich, R.; Hilbert, H.; Piagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.  
 Nucleic Acids Res. 24, 4420-4449, 1996  
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia  
 A:Reference number: S73327; MUID:97105885; PMID:8948633  
 A:Accession: S73927  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-104 <HTM>  
 A:Cross-references: EMBL:AE000058; GB:U00089; NID:g1674231; PIDN:AAB96249.1; PID:g16743  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
 C:Genetics:  
 A:Gene: rps8  
 A:Genetic code: SGC3  
 C:Superfamily: Escherichia coli ribosomal protein S18  
 C:Keywords: protein biosynthesis; ribosome

Query Match 60.0%; Score 42; DB 2; Length 104;  
 Best Local Similarity 72.7%; Pred. No. 2.4;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 FLSPYAKLOPR 14  
 Db 63 FLSPYAKLOPR 73

RESULT 6  
 B64210  
 ribosomal protein S18 - Mycoplasma genitalium  
 C:Species: Mycoplasma genitalium  
 C:Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 07-Dec-1999  
 C:Accession: B64210  
 R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.  
 M.; Fuhmann, J.; Nguyen, D.; Usterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
 C.A.; Venter, J.C.  
 Science 270, 397-403, 1995  
 A:Title: The minimal gene complement of Mycoplasma genitalium.  
 A:Reference number: A64200; MUID:96026346; PMID:7569993  
 A:Accession: B64210  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-105 <TTGR>  
 A:Cross-references: GB:U39688; GB:U43967; NID:g1045753; PID:g1045769; TIGR:MG092  
 A:Experimental source: strain G-37  
 C:Genetics:  
 A:Genetic code: SGC3  
 A:Start codon: GTG  
 C:Superfamily: Escherichia coli ribosomal protein S18

Query Match 60.0%; Score 42; DB 2; Length 105;  
 Best Local Similarity 72.7%; Pred. No. 2.4;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 FLSPYAKLOPR 14  
 Db 64 FLSPYAKLOPR 74

RESULT 7  
 T23249  
 hypothetical protein K02E2.7 - Caenorhabditis elegans

```

C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T23249
R/Lloyd, C.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19716
A/Accession: T23249
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-164 <MTL>
A/Cross-references: EMBL:Z81560; PIDN:CAB04544.1; GSPDB:GN00023; CESP:K02E2.7
A/Experimental source: clone K02E2
C/Genetics:
A/Gene: CESP:K02E2.7
A/Map position: 5
A/Introns: 35/1; 62/1

Query Match
Best Local Similarity 58.6%; Score 41; DB 2; Length 164;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSFLSPKALQ 13
|:|:|:|:|:|
Db 3 SNFKSPPELQ 14

RESULT 8
S34851
hypothetical 31.9K protein - Streptomyces lavendulae plasmid pSLG33
C/Species: Streptomyces lavendulae
C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Sep-1999
C/Accession: S34851
R/Feliseberg, J.; Petricek, M.; Tichy, P.
Nucleic Acids Res. 21, 3582, 1993
A/Title: Nucleotide sequence of the mini-plasmid pSLG33 from Streptomyces lavendulae-gra
A/Reference number: S34850; MUID:93348001; PMID:8346038
A/Accession: S34851
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-283 <FEL>
A/Cross-references: EMBL:X69872
C/Genetics:
A/Genome: plasmid pSLG33
A/Supfamily: Streptomyces lavendulae plasmid pSLG33 hypothetical 31.9K protein

Query Match
Best Local Similarity 58.6%; Score 41; DB 2; Length 283;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GSSFLSPKALQ 13
|:|:|:|:|:|
Db 64 GKDFLSPETKKP 76

RESULT 9
H87334
conserved hypothetical protein CC0691 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: H87334
R/Nierman, W.C.; Feildlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: H87334
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-208 <STO>
A/Cross-references: GB:AE005673; NID:g13421912; PIDN:AAK22676.1; GSPDB:GN00148
C/Genetics:
A/Gene: CC0691

```

```

Query Match
Best Local Similarity 57.1%; Score 40; DB 2; Length 208;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSSFLSPKALQ 13
|:|:|:|:|:|
Db 108 GATFLNPEARSGP 120

RESULT 10
H87306
glycosyl transferase family protein CC0465 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: H87306
R/Nierman, W.C.; Feildlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: H87306
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-308 <STO>
A/Cross-references: GB:AE005673; NID:g13421638; PIDN:AAK22452.1; GSPDB:GN00148
C/Genetics:
A/Gene: CC0465

Query Match
Best Local Similarity 57.1%; Score 40; DB 2; Length 308;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 FLSPKALQ 13
|:|:|:|:|:|
Db 105 FLNPDANLQ 114

RESULT 11
AB1086
ATP synthase delta chain homolog lmo0089 [imported] - Listeria monocytogenes (strain EGI
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C/Accession: AB1086
R/Glaeser, P.; Frangoul, L.; Buchliesser, C.; Amend, A.; Baguero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurguet, O.; Entian, K.D.; Fsihl, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maltournam, A.; M
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:2157279; PMID:11679669
A/Accession: AB1086
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-343 <GLA>
A/Cross-references: GB:INC_003210; PIDN:G16409448; GSPDB:GN00177
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: lmo0089

Query Match
Best Local Similarity 57.1%; Score 40; DB 2; Length 343;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSFLSPKALQ 12
|:|:|:|:|:|
Db 214 SSYLSPKQKX 224

RESULT 12
AH1449

```

Weakly ATP synthase delta chain homolog 11n0135 [imported] - *Listeria innocua* (strain C)  
 C:Species: *Listeria innocua*  
 C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
 C:Accession: AH1449  
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Feigl, H. Science 294, 849-852, 2001  
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Knapkat, G.; Madueno, E.; Maitourram, A.; Maok, C.; Schuster, T.; Simoes, N.; Teller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomes of *Listeria* species.  
 A:Reference number: AB1077; MUID:21537279; PMID:11679669  
 A:Accession: AH1449  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-343 <GLA>  
 A:Cross-references: GB:AL592022; PIDN:CA95368.1; PID:G16412554; GSPDB:GN00178  
 A:Experimental source: strain C11p11262  
 C:Genetic8:  
 A:Gene: 11n0135

Query Match 57.1%; Score 40; DB 2; Length 343;  
 Best Local Similarity 72.7%; Pred. No. 20;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SFSLSPKALQ 12  
 ||| ||| |||  
 Db 214 SFYSPKQK 224

## RESULT 13

TWBY55  
 Transcription factor SWIS [validated] - Yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: protein YD8358.03c; protein YDR146c  
 C:Species: *Saccharomyces cerevisiae*  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000  
 C:Accession: S00342; S57973  
 R:Stillman, D.J.; Bankier, A.T.; Seddon, A.; Groenhout, E.G.; Nasmyth, K.A. EMBO J. 7, 485-494, 1988  
 A:Title: Characterization of a transcription factor involved in mother cell specific tra  
 A:Reference number: S00342; MUID:88211561; PMID:3284746  
 A:Accession: S00342  
 A:Molecule type: DNA  
 A:Residues: 1-709 <STT>  
 A:Cross-references: EMBL:X06978; NID:G4595; PIDN:CAA30040.1; PID:G4596  
 R:Murphy, L.; Richards, C.; Harris, D.  
 Submitted to the EMBL Data Library, July 1995  
 A:Reference number: S57971  
 A:Accession: S57973  
 A:Molecule type: DNA  
 A:Residues: 1-709 <MUR>  
 A:Cross-references: EMBL:Z50046; NID:G899393; PIDN:CAA90369.1; PID:G899396; GSPDB:GN0000  
 A:Experimental source: strain AB972  
 R:Dutnall, R.N.; Neuhaus, D.; Rhodes, D.  
 Submitted to the Brookhaven Protein Data Bank, February 1996  
 A:Reference number: A66200; PDB:1NCS  
 A:Contents: annotation; conformation by (1)H-NMR, residues 532-578  
 R:Neuhaus, D.; Nakaseko, Y.; Schwabe, J.W.R.; Rhodes, D.; Klug, A.  
 Submitted to the Brookhaven Protein Data Bank, April 1996  
 A:Reference number: A67819; PDB:1ZPD  
 A:Contents: annotation; conformation by (1)H-NMR, residues 577-608  
 R:Nakaseko, Y.; Neuhaus, D.; Klug, A.; Rhodes, D.  
 J. Mol. Biol. 228, 619-636, 1992  
 A:Title: Adjacent zinc-finger motifs in multiple zinc-finger peptides from SWIS form str  
 A:Reference number: A58624; MUID:93085740; PMID:1453467  
 A:Residues: 1-371 <ALC>  
 R:Neuhaus, D.; Nakaseko, Y.; Schwabe, J.W.R.; Klug, A.  
 J. Mol. Biol. 228, 637-651, 1992  
 A:Title: Solution structures of two zinc-finger domains from SWIS obtained using two-dim  
 C:Reference number: A58623; MUID:93085741; PMID:1453468  
 A:Contents: annotation; conformation by (1)H-NMR  
 C:Comment: This protein activates the HO gene, which codes for an endonuclease responsib

C:Genetics:  
 A:Gene: SGD:SWIS; MIPS:YDR146C  
 A:Cross-references: SGD:S0002553; MIPS:YDR146C  
 A:Map position: 4R  
 C:Superfamily: transcription factor SWIS  
 C:Keywords: DNA binding; metalloprotein; transcription factor; zinc finger  
 F:550-574/Region: zinc finger CCH motif  
 F:580-604/Region: zinc finger CCH motif  
 F:609-632/Region: zinc finger CCH motif  
 F:552,557,570,574/Binding site: zinc (Cys, Cys, His, His) #status experimental  
 F:582,587,600,604/Binding site: zinc (Cys, Cys, His, His) #status experimental  
 F:611,613,626,632/Binding site: zinc (Cys, Cys, His, Cys) #status experimental

Query Match 57.1%; Score 40; DB 1; Length 709;  
 Best Local Similarity 53.8%; Pred. No. 45;  
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GSSFLSPKALQ 13  
 ||| ||| |||  
 Db 220 GQFLSPKRLSP 232

## RESULT 14

MGNZBR  
 major surface glycoprotein G - bovine respiratory syncytial virus (strain 391-2)  
 N:Alternate names: attachment glycoprotein G  
 C:Species: bovine respiratory syncytial virus  
 C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Jul-1999  
 C:Accession: A36408  
 R:Leich, R.A.; Anderson, K.; Wertz, G.W. J. Virol. 64, 5559-5569, 1990  
 A:Title: Nucleotide sequence analysis and expression from recombinant vectors demonstra  
 Y syncytial virus.  
 A:Reference number: A36408; MUID:91012801; PMID:2214024  
 A:Accession: A36408  
 A:Molecule type: mRNA  
 A:Residues: 1-257 <LBR>  
 A:Cross-references: GB:M58307; NID:G210830; PIDN:AAA42810.1; PID:G210831  
 C:Genetics:  
 A:Gene: G  
 C:Superfamily: respiratory syncytial virus major surface glycoprotein G  
 C:Keywords: glycoprotein; transmembrane protein  
 F:45-62/Domain: transmembrane #status predicted <TMN>  
 F:3,85,127,149,233,251/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 55.7%; Score 39; DB 1; Length 257;  
 Best Local Similarity 77.8%; Pred. No. 22;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 SPEAKLQPR 14  
 ||| ||| |||  
 Db 224 SPEKLOPK 232

## RESULT 15

T49100  
 hypothetical protein P4F15.320 - *Arabidopsis thaliana*  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
 C:Accession: T49100  
 R:Alcazar, J.P.; Clabault, G.; Cottet, A.; Maché, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.  
 Submitted to the Protein Sequence Database, April 2000  
 A:Reference number: Z25015  
 A:Accession: T49100  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-371 <ALC>  
 A:Cross-references: EMBL:AL049711; GSPDB:GN00061; ATSP:P4F15.320  
 A:Experimental source: cultivar Columbia; BAC clone P4F15  
 C:Genetics:  
 A:Gene: ATSP:P4F15.320  
 A:Map position: 3  
 A:introns: 34/3; 61/1; 100/1; 151/2; 182/2; 222/2; 252/1; 297/3

Query Match 55.7%; Score 39; DB 2; Length 371;  
 Best Local Similarity 50.0%; Pred. No. 34;  
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GSSFLSPPEAKIQPR 14  
 DB 233 GPNFVDPGRKLLPR 246

Search completed: January 29, 2003, 13:23:59  
 Job time : 16 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2003, 12:58:36 ; Search time 11 Seconds

(without alignments)  
52.788 Million cell updates/sec

Title: MAYES-902-SEQ1

Perfect score: 70

Sequence: 1 gseflpeaklqpr 14

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	53	75.7	117	1	GHRL_CANFA	Q9b6f8 canis fam1
2	53	75.7	117	1	GHRL_HUMAN	Q9ubd3 homo sapien
3	53	75.7	117	1	GHRL_MOUSE	Q9eqx0 mus musculi
4	53	75.7	117	1	GHRL_RAT	Q9qy17 rattus norv
5	49	70.0	118	1	GHRL_PIG	Q9qky5 sus scrofa
6	43	61.4	257	1	VGIG_BRSV7	Q65706 bovine resp
7	43	61.4	257	1	VGIG_BRSVL	Q09495 bovine resp
8	43	61.4	257	1	VGIG_BRSVR	Q84183 bovine resp
9	42.5	60.7	116	1	GHRL_BOVIN	Q9bd16 bos taurus
10	42	60.0	104	1	RS18_MYCPN	P75541 mycoplasma
11	42	60.0	105	1	RS18_MYCBE	P47338 mycoplasma
12	40	57.1	369	1	V181_FOPPV	Q91552 fowpox vir
13	40	57.1	709	1	SWIS_YEAST	P08183 saccharomyc
14	39.5	56.4	309	1	ID12_CANAC	Q48965 campotheca
15	39	55.7	257	1	VGIG_BRSCV	P22261 bovine resp
16	39	55.7	559	1	HNFB_MOUSE	P27889 mus musculi
17	39	55.7	742	1	KM65_YEAST	Q03656 saccharomyc
18	38	54.3	154	1	FEA2_ECOLI	P53599 escherichia
19	38	54.3	961	1	BASO_MOUSE	Q35914 mus musculi
20	38	54.3	994	1	BASO_HUMAN	Q01954 homo sapien
21	37	52.9	154	1	FEA1_ECOLI	P53508 escherichia
22	37	52.9	183	1	PDA2_METWA	P58890 methanobact
23	37	52.9	309	1	CBPC_RAT	P21961 rattus norv
24	37	52.9	417	1	CBPC_MOUSE	P15089 mus musculi
25	37	52.9	1152	1	MAP4_HUMAN	P27816 homo sapien
26	37	52.9	1495	1	A2MG_MOUSE	Q61838 mus musculi
27	36	51.4	263	1	LPXA_CAUCR	Q94715 caulobacter
28	36	51.4	263	1	VGIG_BRSVW	Q10687 bovine resp
29	36	51.4	382	1	ISCC_ARCFU	Q29669 archaeoglob
30	36	51.4	465	1	YHCL_YEAST	P33180 saccharomyc
31	36	51.4	1057	1	SEF1_YEAST	P34228 saccharomyc
32	36	51.4	1072	1	MAP4_BOVIN	P36225 bos taurus
33	36	51.4	1402	1	IF4G_RABIT	P41110 oryctolagus

34	36	51.4	1581	1	ARO1_PNECA	Q12559 p pentafunc
35	36	51.4	1787	1	CHD3_CAEBL	Q22516 caenorhabdi
36	35.5	50.7	405	1	FLIG_BUCAL	P57422 buchnera ap
37	35	50.0	263	1	VGIG_BRSVL	Q10683 bovine resp
38	35	50.0	263	1	VGIG_BRSV2	Q10685 bovine resp
39	35	50.0	263	1	VGIG_BRSV4	Q10684 bovine resp
40	35	50.0	295	1	UL79_HCMVA	P16752 human cytom
41	35	50.0	355	1	LPXD_AGRTS	Q84f15 agrobacteri
42	35	50.0	394	1	ARP2_CHICK	P53488 gallus gall
43	35	50.0	394	1	ARP2_HUMAN	O15142 homo sapien
44	35	50.0	395	1	ARP2_DROME	P45868 drosophila
45	35	50.0	559	1	HNFB_PIG	Q03365 sus scrofa

## ALIGNMENTS

RESULT 1  
GHRL\_CANFA STANDARD; PRT; 117 AA.  
AC Q9b6f8; Q9b6f7;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).  
GN GHRL\_OR\_MTLRP.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Gastric fundus;  
RA Tomasetto C., Wendling C., Rio M.-C., Poltrae P.;  
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog fundus."  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1/ghrelin (shown here) and 2/ghrelin-ghrelin; are produced by alternative splicing.  
CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; A0298295; CAC29155.1; -;  
DR EMBL; A0298296; CAC29156.1; -;  
KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;  
KW Alternative splicing.  
FT SIGNAL 1 23 BY SIMILARITY.  
FT PEPTIDE 24 51 GHRELIN (BY SIMILARITY).  
FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).  
FT LIPID 26 26 N-OCTANOATE (BY SIMILARITY).  
FT VARSPIC 37 37 MISSING (IN ISOFORM 2).  
SQ SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;  
Query Match 75.7%; Score 53; DB 1; Length 117;  
Best Local Similarity 50.0%; Pred. No. 0.012; Indels 14; Gaps 1;  
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
QY 1 GSSFLSPK-----AKQPR 14

```

Db      24 GSSFLSPHQKLRQKSKKPKLQPR 51
|||||
RESULT 2
GHR_L_HUMAN  STANDARD;  PRT;  117 AA.
ID  GHR_L_HUMAN
AC  Q9UBJ3; Q9UBJ3;
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
GN  releasing peptide) (Motilin-related peptide) (M46 protein).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SPR-26.
RX  MEDLINE=20067959; PubMed=10604470;
RA  Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT  "Ghrelin is a growth-hormone-releasing acylated peptide from
RL  stomach."
RN  [2]
RP  NATURE 402:656-660 (1999).
RN  [3]
RP  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA  Kojima M.;
RT  Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN  [4]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RT  TISSUE=Stomach;
RA  Tomasetto C., Karam S.M., Rio M.-C.;
RT  "Identification of a novel gastric protein m46."
RN  [5]
RP  Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN  [6]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RA  Wajsbach M.P., Ten I.S., Gertner J.M., Leibel R.L.;
RT  "Genomic organization of the human Ghrelin gene."
RN  [7]
RP  J. Endocrinol. Genet. 1:231-233 (2000).
RN  [8]
RP  SEQUENCE OF 24-33.
RN  [9]
RP  TISSUE=Stomach;
RX  MEDLINE=20389976; PubMed=10930375;
RA  Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RT  Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT  "Identification and characterization of a novel gastric peptide
RL  hormone: the motilin-related peptide."
RN  [10]
RP  Gastroenterology 119:395-405 (2000).
RN  [11]
RP  REVIEW.
RX  MEDLINE=21203998; PubMed=11306336;
RA  Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT  "Ghrelin: discovery of the natural endogenous ligand for the growth
RT  hormone secretagogue receptor."
RL  Trends Endocrinol. Metab. 12:118-122 (2001).
RN  [12]
RP  FUNCTION: Specific ligand for the growth hormone secretagogue
CC  receptor type 1 (GHSR) inducing the release of growth hormone from
CC  the pituitary. Has an appetite-stimulating effect, induces
CC  adiposity and stimulates gastric acid secretion. Involved in
CC  growth regulation.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/ghrelin (shown here) and
CC  2/dea-Gln4-ghrelin; are produced by alternative splicing.
CC  -1- PTM: O-n-octanoylation is essential for activity.
CC  -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC  -1- DATABASE: NAME=Acids Genet. CytoGenet. Oncol. Haematol.;
CC  WWW="http://www.infobiogen.fr/services/chromocancer/Genes/GhrelinD.html".
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR  EMBL; AB029434; BAA89371.1; -
DR  EMBL; AB035700; BAB19045.1; -
DR  EMBL; AJ252278; CAB65733.1; -
DR  EMBL; AF296558; AAG10300.1; -
DR  MIM; 605353; -
KW  Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;
KW  Alternative splicing.
FT  SIGNAL 1
FT  PEPTIDE 24 51 GHRELIN.
FT  PROPEP 52 117 REMOVED IN MATURE FORM.
FT  LIPID 26
FT  VASPLIC 37 37 MISSING (IN ISOFORM 2).
SQ  SEQUENCE 117 AA; 12911 MW; 39C0572BBECA2755 CRC64;

Query Match 75.7%; Score 53; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 0.012;
Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

Qy 1 GSSFLSP-----AKLQPR 14
Db 24 GSSFLSPHQKLRQKSKKPKLQPR 51
|||||
RESULT 3
GHR_L_MOUSE  STANDARD;  PRT;  117 AA.
ID  GHR_L_MOUSE
AC  Q9EQX0; Q9WU21;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE  releasing peptide) (Motilin-related peptide) (M46 protein).
GN  GHR_L OR MTLRP.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30.
RN  [2]
RP  TISSUE=Stomach;
RX  MEDLINE=20389976; PubMed=10930375;
RA  Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RT  Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT  "Identification and characterization of a novel gastric peptide
RT  hormone: the motilin-related peptide."
RN  [3]
RP  Gastroenterology 119:395-405 (2000).
RN  [4]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RA  Kojima M.;
RT  "Mouse mRNA for preproghrelin."
RN  [5]
RP  Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN  [6]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RA  Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakaishima K.;
RT  Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN  [7]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RX  STRAIN=C57BL/6J; TISSUE=Stomach;
RX  MEDLINE=21085660; PubMed=11217811;
RA  Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA  Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA  Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

```

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombasets P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.",  
 RL Nature 409:685-690(2001).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=21203998; PubMed=11306336;  
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;  
 RT "ghrelin: discovery of the natural endogenous ligand for the growth  
 hormone secretagogue receptor.";  
 RL Trends Endocrinol. Metab. 12:118-122(2001).  
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue  
 CC receptor type 1 (GHSR) inducing the release of growth hormone from  
 CC the pituitary. Has an appetite-stimulating effect, induces  
 CC adiposity and stimulates gastric acid secretion. Involved in  
 CC growth regulation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/ghrelin (shown here) and  
 CC 2/dea-Gln14-ghrelin; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract  
 CC with higher levels in the stomach, medium levels in the duodenum,  
 CC jejunum, ileum and colon. Low expression in the testis and brain.  
 CC Not detected in the salivary gland, pancreas, liver and lung.  
 CC -1- PTM: O-n-octanoylation is essential for activity (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AJ243503; CAB46500.1; -  
 DR EMBL; AB035701; BAB19046.1; -  
 DR EMBL; AB060078; BAB69857.1; -  
 DR EMBL; AK008658; BAB25814.1; -  
 DR EMBL; AK008660; BAB25934.1; -  
 DR MGI; MGI:193008; Mclrp.  
 KW Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;  
 KW Alternative splicing.  
 FT SIGNAL 1 23  
 FT PEPTIDE 51 GHRELIN.  
 FT PROPEP 52 117 REMOVED IN MATURE FORM (BY SIMILARITY).  
 FT LIPID 26 N-OCTANOATE (BY SIMILARITY).  
 FT VARSPIC 37 37 MISSING (IN ISOFORM 2).  
 SQ SEQUENCE 117 AA; 13207 MW; EACBA9D2E3CA7203 CRC64;  
 Query Match 75.7%; Score 53; DB 1; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.012; Mismatches 14; Gaps 1;  
 Matches 14; Conservative 0; Indels 14; Gaps 1;  
 QY 1 GGSFLSPS-----AKQPR 14  
 DB 24 GGSFLSPSHQRAQORKESSKPPAKQPR 51  
 RESULT 4  
 GHR\_L\_RAT STANDARD; PRT; 117 AA.  
 ID GHR\_L\_RAT  
 AC Q9QYH7; Q9ETE9;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone  
 releasing peptide).

GN GHR\_L.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 24-51, MASS SPECTROMETRY,  
 RP AND ACYLATION OF SER-26.  
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;  
 RX MEDLINE=20067959; PubMed=10604470;  
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;  
 RT "ghrelin is a growth-hormone-releasing acylated peptide from  
 RT stomach.";  
 RL Nature 402:656-660(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS  
 RP SPECTROMETRY, AND ACYLATION OF SER-26.  
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;  
 RX MEDLINE=20357315; PubMed=10801861;  
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;  
 RT "Purification and characterization of rat dea-Gln14-ghrelin, a second  
 RT endogenous ligand for the growth hormone secretagogue receptor.";  
 RL J. Biol. Chem. 275:21995-22000(2000).  
 RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=21092536; PubMed=1162448;  
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;  
 RT "ghrelin and dea-acyl ghrelin: two major forms of rat ghrelin peptide  
 RT in gastrointestinal tissue.";  
 RL Biochem. Biophys. Res. Commun. 279:909-913(2000).  
 RN [4]  
 RP STRUCTURE-ACTIVITY RELATIONSHIP.  
 RX MEDLINE=2143488; PubMed=11549267;  
 RA Matsumoto M., Hosoda H., Kiritajima Y., Morozumi N., Minamitake Y.,  
 RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;  
 RT "Structure-activity relationship of ghrelin: pharmacological study of  
 RT ghrelin peptides.";  
 RL Biochem. Biophys. Res. Commun. 287:142-146(2001).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=21203998; PubMed=11306336;  
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;  
 RT "ghrelin: discovery of the natural endogenous ligand for the growth  
 RT hormone secretagogue receptor.";  
 RL Trends Endocrinol. Metab. 12:118-122(2001).  
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue  
 CC receptor type 1 (GHSR) inducing the release of growth hormone from  
 CC the pituitary. Has an appetite-stimulating effect, induces  
 CC adiposity and stimulates gastric acid secretion. Involved in  
 CC growth regulation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/ghrelin (shown here) and  
 CC 2/dea-Gln14-ghrelin; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Broadly expressed with higher expression in  
 CC the stomach. Very low levels are detected in the hypothalamus,  
 CC heart, lung, pancreas, intestine and adipose tissue.  
 CC -1- PTM: O-n-octanoylation is essential for activity. The replacement  
 CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.  
 CC -1- MASS SPECTROMETRY: MW=3314.9; MW\_ERR=0.7; METHOD=Electrospray;  
 CC RANGE=24-51.  
 CC -1- MASS SPECTROMETRY: MW=3187.1; MW\_ERR=0.6; METHOD=Electrospray;  
 CC RANGE=24-36, 38-51.  
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AB029433; BAA89370.1; -

DR EMBL; AB035699; BAB1956.1; -  
 KM Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;  
 KW Alternative splicing.  
 FT SIGNAL 1 23  
 FT PEPTIDE 24 51 GHRELIN  
 FT PROPEP 52 117 REMOVED IN MATURE FORM.  
 FT LIPID 26 26 N-OCTANOATE.  
 FT VARSPPLIC 37 37 MISSING (IN ISOFORM 2).  
 SQ SEQUENCE 117 AA; 13176 MW; 8857546F5E1A7691 CRC64;  
 Query Match 75.7%; Score 53; DB 1; Length 117;  
 Best Local Similarity 50.0%; Pred. No. 0.012;  
 Matches 14; Conservative 0; Mismatches 0; Indels 14; Gaps 1;  
 Oy 1 GSSFLSPPE-----AKLOPR 14  
 |||||  
 Db 24 GSSFLSPPEHQKQKRSKKPKAKQPR 51  
 |||||  
 RESULT 5  
 GHRL\_PIG STANDARD; PRT; 118 AA.  
 ID GHRL\_PIG  
 AC 09GKY5; 09GKY4; 09BDG8;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide).  
 GN GHRL.  
 OS Sue scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_Taxid=9923;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RA Kojima M.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Stomach;  
 RA Rousselet J.; Lacroix D.; Dubreuil P.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/ghrelin (shown here) and 2/dea-Gln14-ghrelin; are produced by alternative splicing.  
 CC -1- PFM: O-n-octanoylation is essential for activity (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; AB035703; BAB19048.1; -  
 DR EMBL; AB035704; BAB19049.1; -  
 DR EMBL; AF308930; AAK19243.1; -  
 DR EMBL; AY028942; AAK30002.1; -  
 KM Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein;  
 KW Alternative splicing.  
 FT SIGNAL 1 24  
 FT PEPTIDE 25 52 GHRELIN.  
 FT PROPEP 53 118 REMOVED IN MATURE FORM (BY SIMILARITY).  
 FT LIPID 27 27 N-OCTANOATE (BY SIMILARITY).  
 FT VARSPPLIC 38 38 MISSING (IN ISOFORM 2).  
 FT CONFLICT 17 17 L -> P (IN REF. 2; AAK30002).  
 FT CONFLICT 17 17

FT CONFLICT 72 72 K -> E (IN REF. 2; AAK30002).  
 SQ SEQUENCE 118 AA; 12785 MW; 856D3E1D6DB1A76 CRC64;  
 Query Match 70.0%; Score 49; DB 1; Length 118;  
 Best Local Similarity 46.4%; Pred. No. 0.064;  
 Matches 13; Conservative 1; Mismatches 0; Indels 14; Gaps 1;  
 Oy 1 GSSFLSPPE-----AKLOPR 14  
 |||||  
 Db 25 GSSFLSPPEHQKQKRSKKPKAKTKPR 52  
 |||||  
 RESULT 6  
 VGLG\_BRSV7 STANDARD; PRT; 257 AA.  
 ID VGLG\_BRSV7  
 AC 065706;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Major surface glycoprotein G (Attachment glycoprotein G).  
 GN G.  
 OS Bovine respiratory syncytial virus (strain 375) (BRV).  
 CC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 CC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_Taxid=82821;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Duncan R.B.; Potgieter L.N.D.;  
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTININATING ACTIVITIES.  
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.  
 CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; L10925; AAA42809.1; -  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot\_G.  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 KM Transmembrane; Glycoprotein.  
 FT DOMAIN 1 37  
 FT TRANSMEM 38 66  
 FT DOMAIN 1 37  
 FT TRANSMEM 38 66  
 FT DOMAIN 1 37  
 FT TRANSMEM 38 66  
 FT DISULFID 173 257  
 FT DISULFID 176 182  
 FT CARBOHYD 85 85  
 FT CARBOHYD 163 163  
 FT CARBOHYD 233 233  
 FT CARBOHYD 248 248  
 FT CARBOHYD 251 251  
 SQ SEQUENCE 257 AA; 28363 MW; F7CE3396305CC015 CRC64;  
 Query Match 61.4%; Score 43; DB 1; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 1.8;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 6 SPEAKIQPR 14  
 |||||  
 Db 224 SPEAKIQPK 232  
 |||||  
 RESULT 7  
 VGLG\_BRSVL

```

ID  VGLG_BRSVL  STANDARD;  PRT;  257 AA.
AC  009495;
DT  15-JUL-1998 (Rel. 36, Created)
DT  15-JUL-1998 (Rel. 36, Last sequence update)
DE  15-JUL-1998 (Rel. 36, Last annotation update)
DE  Major surface glycoprotein G (Attachment glycoprotein G).
GN  G.
OS  Bovine respiratory syncytial virus (strain LeJesteau) (BRV).
OC  Viruses; ssRNA negative-strand viruses; Mononegavirales;
OX  Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=82823;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9710754; PubMed=9018058;
RA  Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,
RT  Letesson J.J.;
RT  "Antigenic and molecular analyses of the variability of bovine
RT  respiratory syncytial virus G glycoprotein.";
RL  J. Gen. Virol. 78:359-366(1997).
CC  -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC  HEMAGGLUTININATING ACTIVITIES.
CC  -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC  -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
CC  HRS VIRUS.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL; U35339; AAB50935.1; -.
DR  HSSP; P22261; 1BRV.
DR  InterPro; IPR000925; Glycoprot G.
DR  Pfam; PF00802; Glycoprotein_G; 1.
KM  Transmembrane; Glycoprotein.
FT  DOMAIN 1 37
FT  TRANSMEM 38 66
FT  DOMAIN 67 257
FT  DISULFID 173 186
FT  CARBOHYD 176 182
FT  CARBOHYD 85 85
FT  CARBOHYD 163 163
FT  CARBOHYD 233 233
FT  CARBOHYD 251 251
SQ  SEQUENCE 257 AA; 28354 MW; 8BD5710FB21ACDA CRC64;

Query Match 61.4%; Score 43; DB 1; Length 257;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKQPR 14
   |||||:
   |||||:
Db 224 SPEAKQPK 232

```

```

OX  NCBI_TaxID=11249, 82822;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=RB94;
RX  MEDLINE=9710754; PubMed=9018058;
RA  Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,
RT  Letesson J.J.;
RT  "Antigenic and molecular analyses of the variability of bovine
RT  respiratory syncytial virus G glycoprotein.";
RL  J. Gen. Virol. 78:359-366(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  STRAIN=220-69;
RX  MEDLINE=97288324; PubMed=9143302;
RA  Furze J., Roberts S., Wertz G., Taylor G.;
RT  "Antigenically distinct G glycoproteins of BRSV strains share a high
RT  degree of genetic homogeneity.";
RL  Virology 231:48-58(1997).
CC  -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC  HEMAGGLUTININATING ACTIVITIES.
CC  -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC  CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC  -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
CC  HRS VIRUS.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL; L27802; AAB47926.1; -.
DR  EMBL; Y08720; CAA69970.1; -.
DR  HSSP; P22261; 1BRV.
DR  InterPro; IPR000925; Glycoprot G.
DR  Pfam; PF00802; Glycoprotein_G; 1.
KM  Transmembrane; Glycoprotein.
FT  DOMAIN 1 37
FT  TRANSMEM 38 66
FT  DOMAIN 67 257
FT  DISULFID 173 186
FT  CARBOHYD 176 182
FT  CARBOHYD 85 85
FT  CARBOHYD 163 163
FT  CARBOHYD 233 233
FT  CARBOHYD 251 251
SQ  SEQUENCE 257 AA; 28388 MW; D93E5347FA25FEFF CRC64;

Query Match 61.4%; Score 43; DB 1; Length 257;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKQPR 14
   |||||:
   |||||:
Db 224 SPEAKQPK 232

```

```

RESULT 8
VGLG_BRSVR  STANDARD;  PRT;  257 AA.
AC  084183; 012865; 012584;
DT  15-JUL-1998 (Rel. 36, Created)
DT  15-JUL-1998 (Rel. 36, Last sequence update)
DT  15-JUL-1998 (Rel. 36, Last annotation update)
DE  Major surface glycoprotein G (Attachment glycoprotein G).
GN  G.
OS  Bovine respiratory syncytial virus (strain RB94) (BRV), and
OS  Bovine respiratory syncytial virus (strain 220-69) (BRV).
OC  Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC  Paramyxoviridae; Pneumovirinae; Pneumovirus.

```

```

RESULT 9
GHRL_BOVIN  STANDARD;  PRT;  116 AA.
AC  09BD76; 09GKY6;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE  releasing peptide).
GN  GHRL.
OS  Bos taurus (Bovine).
OS  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

```

```

CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Kita K., Harada K., Yokota H.
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-99 FROM N.A.
RA Kojima M.
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
    receptor type 1 (GHR) inducing the release of growth hormone from
    the pituitary. Has an appetite-stimulating effect. Induces
    adiposity and stimulates gastric acid secretion. Involved in
    growth regulation (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF350329; AAK18612.1;
DR EMBL: AB035702; BAB19047.1;
DR Hormone; Cleavage on pair of basic residues; Signal; Lipoprotein.
FT SIGNAL 1 23
FT PESTIDE 24 50
FT PROPEP 51 116
FT LIPID 26 26
FT CONFLICT 34 34
FT SEQUENCE 116 AA; 12792 MW; F55356DAC5FA59B6 CRC64;
SQ
Query Match 60.7%; Score 42.5; DB 1; Length 116;
Best Local Similarity 84.6%; Pred. No. 0.95;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 GSSFLSPF-AKIQ 12
DQ 24 GSSFLSPFHQKQ 36
RESULT 10
RS18_MYCEN STANDARD; PRT; 104 AA.
AC P75541;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S18.
GN RPSR OR MPN230 OR MP601.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 29342 / M129;
RA MEDLINE=97105885; PubMed=8948633;
RA Himmelfreid R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Hermann R.
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
    pneumoniae."
RL Nucleic Acids Res. 24:4420-4449 (1996).
CC -1- FUNCTION: This protein has been implicated in aminoacyl-transfer
    RNA binding. It appears to be situated at the decoding site of
    messenger RNA (By similarity).
CC -1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC -----

```

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000059; AAB96249.1;
DR InterPro: IPR001648; Ribosomal S18.
DR Pfam: PFO1084; Ribosomal S18; I.
DR PRINTS: PR00974; RIBOSOMALS18.
DR ProDom: PD002239; Ribosomal S18; 1.
DR TIGRPFAMs: TIGR00165; S18; 1.
DR PROSITE: PS00057; RIBOSOMAL_S18; FALSE NEG.
KW Ribosomal protein; RNA-binding; Complete proteome.
SQ SEQUENCE 104 AA; 12386 MW; 0C424229C79CC1B5 CRC64;
OY 4 FLSPDAKQPR 14
DQ 63 FLSPYAKINPR 73
RESULT 11
RS18_MYCEN STANDARD; PRT; 105 AA.
AC P47338;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S18.
GN RPSR OR RPS18 OR MG092.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 33530 / G-37;
RA MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandhu K., Fritchman J.L.,
RA Nguyen D.T., Uettermann T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Luster T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403 (1995).
CC -1- FUNCTION: This protein has been implicated in aminoacyl-transfer
    RNA binding. It appears to be situated at the decoding site of
    messenger RNA (By similarity).
CC -1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U39689; AAC71310.1;
DR TIGR: MG092;
DR InterPro: IPR001648; Ribosomal S18.
DR Pfam: PFO1084; Ribosomal S18; I.
DR PRINTS: PR00974; RIBOSOMALS18.
DR ProDom: PD002239; Ribosomal S18; 1.
DR TIGRPFAMs: TIGR00165; S18; 1.
DR PROSITE: PS00057; RIBOSOMAL_S18; FALSE NEG.
KW Ribosomal protein; RNA-binding; Complete proteome.
SQ SEQUENCE 105 AA; 12463 MW; 0D5F5A1276DF5A26 CRC64;

```

```

Query Match      60.0%; Score 42; DB 1; Length 105;
Best Local Similarity 72.7%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FLSPKATOPR 14
    |||||:
    64 FLSPYAKINPR 74

RESULT 12
ID V181_FOWPV STANDARD; PRT; 369 AA.
AC 09J552;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Protein FFW181.
GN FFW181.
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Afonso C.L., Tulman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC - SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: AF198100; AAF4525.1; -.
CC DR InterPro: IPR004251; DUF230.
CC DR Pfam: PF03003; DUF230; 1.
CC SQ SEQUENCE 369 AA; 42081 MW; 380A71032C18B999 CRC64;

Query Match      57.1%; Score 40; DB 1; Length 369;
Best Local Similarity 88.9%; Pred. No. 9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSFLSPK 10
    |||||
    68 ASFLSPK 76

RESULT 13
ID V181_FOWPV STANDARD; PRT; 709 AA.
AC P08153;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional factor SW15.
GN SW15 OR YDR146C OR YD8358.03C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88211561; PubMed=3284746;
RA Stillman D.J., Bankier A.T., Seddon A., Groenhout E.G., Naamyn K.A.;
RT "Characterization of a transcription factor involved in mother cell
RT specific transcription of the yeast HO gene.";
EMBO J. 7:485-494(1988).

```

```

RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=8288C / AB972;
RA Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP DNA-BINDING.
RX MEDLINE=88156968; PubMed=2831463;
RA Nagai K., Nakaseko Y., Naamyn K.A., Rhodes D.;
RT "Zinc-finger motifs expressed in E. coli and folded in vitro direct
RT specific binding to DNA.";
RL Nature 332:284-286(1988).
RN [4]
RP PHOSPHORYLATION, MUTAGENESIS, AND INTRACELLULAR LOCALIZATION.
RX MEDLINE=91347374; PubMed=1652372;
RA Moll T., Tebb G., Surana U., Robitsek H., Naamyn K.;
RT "The role of phosphorylation and the CDC28 protein kinase in cell
RT cycle-regulated nuclear import of the S. cerevisiae transcription
RT factor SW15.";
RL Cell 66:743-758(1991).
RN [5]
RP STRUCTURE BY NMR OF 540-608.
RX MEDLINE=93085741; PubMed=1453468;
RA Neuhaus D., Nakaseko Y., Schwabe J.W.R., Klug A.;
RT "Solution structures of two zinc-finger domains from SW15 obtained
RT using two-dimensional 1H nuclear magnetic resonance spectroscopy. A
RT zinc-finger structure with a third strand of beta-sheet.";
RL J. Mol. Biol. 228:637-651(1992).
CC - FUNCTION: DETERMINES THE MOTHER-CELL-SPECIFIC TRANSCRIPTION OF THE
CC HO ENDONUCLEASE GENE THAT IS RESPONSIBLE FOR THE INITIATION OF
CC MATING-TYPE SWITCHING IN YEAST. RECOGNIZES A SPECIFIC SEQUENCE IN
CC THE PROMOTER OF THE HO GENE. ACTIVATES EGT2 TRANSCRIPTION IN A
CC CONCENTRATION-DEPENDENT MANNER. SYNTHESIZED DURING G2 AND EARLY
CC MITOSIS.
CC - SUBCELLULAR LOCATION: NUCLEAR IN G1, BUT CYTOPLASMIC IN S, G2, AND
CC M CELL CYCLE PHASES.
CC - PTM: CELL CYCLE-DEPENDENT PHOSPHORYLATION OF THREE SERINE RESIDUES
CC PREVENTS SW15 FROM ENTERING THE NUCLEUS, AND IT ACCUMULATES IN THE
CC CYTOPLASM. AS A CONSEQUENCE OF CDC28 KINASE INACTIVATION AT THE
CC END OF ANAPHASE, THE THREE SERINE RESIDUES ARE DEPHOSPHORYLATED
CC AND SW15 ENTERS THE NUCLEUS TO ACTIVATE TRANSCRIPTION. IT IS THEN
CC RAPIDLY DEGRADED. THREONINE PHOSPHORYLATION ALSO SEEMS TO OCCUR.
CC - SIMILARITY: STRONG, TO YEAST METALLOTHIONEIN EXPRESSION ACTIVATOR
CC ACE2.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: X06978; CAA30040.1; -.
CC DR EMBL: Z50046; CAA90369.1; -.
CC DR PIR: S00342; TWBY55.
CC DR PDB: 1NCS; 10-TUL-96.
CC DR PDB: 1ZFD; 14-OCT-96.
CC DR TRANSPAC: T00776; -.
CC DR SGD: S0002553; SW15.
CC DR InterPro: IPR000637; ZNF_C2H2.
CC DR InterPro: IPR000822; ZNF_C2H2.
CC DR Pfam: PF00096; ZF-C2H2; 3.
CC DR PRINTS: PR02178; AT_hook; 1.
CC DR SMART: SM00384; AT_hook; 1.
CC DR SMART: SM00355; ZNF_C2H2; 2.
CC DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 2.
CC DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 2.
CC DR TRANSCRIPTION REGULATION; Activator; Zinc-finger; DNA-binding;
CC Repeat; Metal-binding; Nuclear protein; Phosphorylation;
CC 3D-structure.

```

```

FT DOMAIN 550 632 ZINC FINGERS.
FT ZN_FING 550 574 C2H2-TYPE.
FT ZN_FING 580 604 C2H2-TYPE.
FT ZN_FING 609 632 C2H2-TYPE.
FT SITE 635 659 NUCLEAR TARGETING SIGNAL (POTENTIAL).
FT MOD_RES 522 522 PHOSPHORYLATION (BY CDC28).
FT MOD_RES 646 646 PHOSPHORYLATION (BY CDC28).
FT MOD_RES 664 664 PHOSPHORYLATION (BY CDC28).
FT MUTAGEN 522 522 S->A: CONSTITUTIVE NUCLEAR ENTRY; WHEN
FT MUTAGEN 646 646 ASSOCIATED WITH A-646 AND A-664.
FT MUTAGEN 664 664 S->A: CONSTITUTIVE NUCLEAR ENTRY; WHEN
FT MUTAGEN 664 664 ASSOCIATED WITH A-522 AND A-664.
FT MUTAGEN 664 664 S->A: CONSTITUTIVE NUCLEAR ENTRY; WHEN
FT MUTAGEN 664 664 ASSOCIATED WITH A-522 AND A-646.
SQ SEQUENCE 709 AA; 79775 MW; BEF5ED5BFB6E30F6 CRC64;

```

```

Query Match 57.1%; Score 40; DB 1; Length 709;
Best Local Similarity 53.8%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Oy 1 GSFSPSPKQLQP 13
Db 220 GPFISPKKISIP 232

```

```

RESULT 14
ID12_CAMAC STANDARD; PRT; 309 AA.
AC 048965-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE isopentenyl-diphosphate delta-isomerase II (EC 5.3.3.2) (IPP isomerase
DE II) (isopentenyl pyrophosphate isomerase II).
GN IRP2.
OS Camptotheca acuminata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Cornales; Cornaceae; Nyssoidae; Camptotheca.
OX NCBI_TaxID=16922;
RN [1]
RP SEQUENCE FROM N.A.
RA Jung K.-H., Christensen D.J., Scott A.I.;
RT "Isolation and characterization of two genes from Camptotheca
RT acuminata that encode isopentenyl diphosphate isomerase.";
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE 1,3-ALLYLIC REARRANGEMENT OF THE
CC HOMOMALLYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS ALLYLIC ISOMER,
CC DIMETHYLLALLYL DIPHOSPHATE (DMAPP) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: isopentenyl diphosphate = dimethylallyl
CC diphosphate.
CC -1- PATHWAY: Chlorophyll biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE IPP ISOMERASE TYPE 1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF031080; AAB94133.1; -.
DR InterPro; IPR002667; IPP_isomerase.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX_1.
DR ProDom; PD004109; IPP_isomerase; 1.
KW isomerase; isoprene biosynthesis; photoynthesis;
KW chlorophyll biosynthesis.
FT ACT_SITE 163 163 BY SIMILARITY.
FT ACT_SITE 225 225 BY SIMILARITY.
SQ SEQUENCE 309 AA; 35205 MW; BAF51CF8D2ED04 CRC64;

```

```

Query Match 56.4%; Score 39.5; DB 1; Length 309;
Best Local Similarity 71.4%; Pred. No. 9.2;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Oy 2 SSFLSPKQLQP 14
Db 16 SSFLASPKLKLHPR 29

```

```

RESULT 15
ID12_CAMAC STANDARD; PRT; 257 AA.
AC P22261.
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Bovine respiratory syncytial virus (strain Copenhagen) (BRV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11248;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91012801; PubMed=2214024;
RA Lerch R.A., Anderson K., Wertz G.W.;
RT "Nucleotide sequence analysis and expression from recombinant vectors
RT demonstrate that the attachment protein G of bovine respiratory
RT syncytial virus is distinct from that of human respiratory syncytial
RT virus."
RL J. Virol. 64:5559-5569(1990).
RN [2]
RP STRUCTURE BY NMR OF 156-189.
RC STRAIN=391-2.
RX MEDLINE=97098087; PubMed=8942628;
RA Dorelajers J.F., Langedijk J.P.M., Haard K., Boelens R.,
RA Rullmann J.A., Schaper W.M., Van Oirschot J.T., Kaptein R.;
RT "Solution structure of the immunodominant region of protein G of
RT bovine respiratory syncytial virus."
RL Biochemistry 35:14684-14688(1996).
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
CC HRS VIRUS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M58307; AAA42810.1; -.
DR PIR; A36408; MGNZER.
DR PDB; 1BRV; 05-JUN-97.
DR InterPro; IPR000925; Glycoprot_G.
DR Pfam; PF00802; Glycoprotein G; 1.
KW Transmembrane; Glycoprotein; 3D-structure.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 257 EXTRACELLULAR (POTENTIAL).
FT DISULFID 173 186
FT DISULFID 176 182
FT CARBOHYD 85 85
FT CARBOHYD 127 127
FT CARBOHYD 233 233
FT CARBOHYD 251 251
SQ SEQUENCE 257 AA; 28569 MW; 0B86D541FBA0657D CRC64;

```



Query Match . 55.7%; Score 39; DB 1; Length 257;  
 Best Local Similarity 77.8%; Pred. No. 9.4;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 SPEAKLOPR 14  
 |||||:  
 Db 224 SPETKLOPK 232

Search completed: January 29, 2003, 13:23:01  
 Job time : 13 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using bw model

Run on: January 29, 2003, 13:19:02 ; Search time 29 Seconds  
(without alignments)  
99.471 Million cell updates/sec

Title: MAYES-902-SEQ1  
Perfect score: 70  
Sequence: 1 gssflspeaklqpr 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp Unclassified:\*  
15: sp\_rvlnus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	75.7	117	4	Q8TAT9
2	43	61.4	251	12	P89309
3	43	61.4	251	12	P90378
4	43	61.4	251	12	P89310
5	43	61.4	257	12	Q9YNF8
6	43	61.4	257	12	Q9YNF9
7	43	61.4	257	12	Q9YNF7
8	43	61.4	257	12	Q9YNF6
9	43	61.4	257	12	Q9YNF5
10	43	61.4	257	12	Q9YNF4
11	43	61.4	257	12	Q9YNF3
12	41	58.6	164	5	Q9XUV5
13	41	58.6	624	11	Q9DBT6
14	41	58.6	815	2	Q47732
15	40	57.1	96	16	Q98F99
16	40	57.1	208	16	Q9AAB3

17	40	57.1	252	2	P70866
18	40	57.1	256	2	Q9S0A7
19	40	57.1	308	16	Q9AAX7
20	40	57.1	343	16	Q92FHI
21	40	57.1	343	16	Q8YAM9
22	40	57.1	470	3	Q8X0Z2
23	40	57.1	680	11	Q921G6
24	40	57.1	1078	5	Q9NDY3
25	39	55.7	188	16	Q92KNO
26	39	55.7	251	12	P89311
27	39	55.7	371	10	Q9SUT4
28	39	55.7	435	11	Q8RI62
29	39	55.7	469	11	Q9CS26
30	39	55.7	473	16	Q9ZC65
31	39	55.7	532	11	Q9RIW2
32	39	55.7	532	11	Q9WTL6
33	39	55.7	558	11	Q9WTL5
34	39	55.7	558	11	Q9RIW1
35	39	55.7	991	5	Q9VIF5
36	39	55.7	1335	11	Q8VIL7
37	39	55.7	1336	11	Q9ES55
38	38.5	55.0	681	10	Q81436
39	38	54.3	103	11	Q8TD22
40	38	54.3	108	10	Q40737
41	38	54.3	187	17	Q970U3
42	38	54.3	226	16	Q9RT86
43	38	54.3	322	5	Q45024
44	38	54.3	406	3	Q9PBD1
45	38	54.3	459	16	Q99U08

## ALIGNMENTS

RESULT 1					
ID	Q8TAT9	PRELIMINARY;	PRT;	117	AA.
AC	Q8TAT9;				
DT	01-JUN-2002 (T-EMBLrel. 21, Created)				
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)				
DT	01-JUN-2002 (T-EMBLrel. 21, Last annotation update)				
DE	Ghrilin.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BLOOD;				
RA	Strausberg R.;				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC025791; AAH25791.1; -				
SQ	SEQUENCE 117 AA; 12929 MW; 25B0572BECB57610 CRC64;				
Query Match					
Best Local Similarity		75.7%;	Score 53;	DB 4;	Length 117;
Matches 14; Conservative 0; Mismatches		50.0%;	Pred. No. 0.031;	0;	Indels 14; Gaps 1;
QY	1 GSSFLSPE-----AKLQPR 14				
DB	24 GSSFLSPEHORVQQRKSKPKPAKLQPR 51				
RESULT 2					
ID	P89309	PRELIMINARY;	PRT;	251	AA.
AC	P89309;				
DT	01-MAY-1997 (T-EMBLrel. 03, Created)				
DT	01-MAY-1997 (T-EMBLrel. 03, Last sequence update)				
DT	01-MAR-2002 (T-EMBLrel. 20, Last annotation update)				
DE	Attachment glycoprotein (Fragment).				
GN	G.				
OS	Bovine respiratory syncytial virus.				

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 NCBI\_TaxId=11246;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=NMK7;  
 MEDLINE=97170754; PubMed=9018058;  
 RA Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,  
 Leloeson J.J.;  
 RT "Antigenic and molecular analyses of the variability of bovine  
 respiratory syncytial virus G glycoprotein.";  
 RL J. Gen. Virol. 78:359-366(1997).  
 DR EMBL; U24713; AAC56940.1; -.  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 251 AA; 27467 MW; CED605DD49103DC3 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 251;  
 Best Local Similarity 88.9%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 218 SPEAKLOPK 226

RESULT 3  
 P90378 PRELIMINARY; PRT; 251 AA.  
 AC P90378;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Attachment glycoprotein (Fragment).  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 NCBI\_TaxId=11246;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=MVS53;  
 MEDLINE=97170754; PubMed=9018058;  
 RA Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,  
 Leloeson J.J.;  
 RT "Antigenic and molecular analyses of the variability of bovine  
 respiratory syncytial virus G glycoprotein.";  
 RL J. Gen. Virol. 78:359-366(1997).  
 DR EMBL; U24714; AAC56941.1; -.  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 251 AA; 27680 MW; 8E11B3B1B0FB8435 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 251;  
 Best Local Similarity 88.9%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 218 SPEAKLOPK 226

RESULT 4  
 P89310 PRELIMINARY; PRT; 251 AA.  
 ID P89310

AC P89310;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Attachment glycoprotein (Fragment).  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 NCBI\_TaxId=11246;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=DORSSET;  
 MEDLINE=97170754; PubMed=9018058;  
 RA Prozzi D., Walravens K., Langedijk J.P., Daus F., Kramps J.A.,  
 Leloeson J.J.;  
 RT "Antigenic and molecular analyses of the variability of bovine  
 respiratory syncytial virus G glycoprotein.";  
 RL J. Gen. Virol. 78:359-366(1997).  
 DR EMBL; U24715; AAC56942.1; -.  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 251 AA; 27643 MW; 7786571D0EFF9D51 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 251;  
 Best Local Similarity 88.9%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 218 SPEAKLOPK 226

RESULT 5  
 Q9YNF9 PRELIMINARY; PRT; 257 AA.  
 AC Q9YNF9;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 NCBI\_TaxId=11246;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RX STRAIN=8307027;  
 MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Utenhental A., Arcander P., Tjornehoj K., Vauff B.,  
 Ronved C., Ronsholt L., Alexandersen S., Blixenkron-Moller M.,  
 RT "Serological and genetic characterization of bovine respiratory  
 syncytial virus (BRV) indicates that Danish isolates belong to the  
 intermediate subgroup: no evidence of a selective effect on the  
 variability of G protein nucleotide sequence by prior cell culture  
 adaptation and passages in cell culture or calves.";  
 RL Vet. Microbiol. 62:265-279(1998).  
 DR EMBL; U92098; AAD00710.1; -.  
 DR HSSP; P22261; 1BRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN\_1.  
 SQ SEQUENCE 257 AA; 28288 MW; C3106210BAC2817 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SPEAKLOPR 14  
 |||||  
 Db 224 SPEAKLOPK 232

## RESULT 6

O9YNF8 PRELIMINARY; PRT; 257 AA.  
 ID O9YNF8;  
 AC O9YNF7;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=87LJ195;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenhal A., Arcander P., Tjornehoj K., Vinuf B.,  
 Ronved C., Ronsholt L., Alexandersen S., Blixenkron-Moller M.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup: no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptation and passages in cell culture or calves.";  
 RL EMBL; U92100; AAD00712.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne\_attach.  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28324 MW; 94EB8BC358739B8 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SPEAKLOPR 14  
 |||||  
 Db 224 SPEAKLOPK 232

## RESULT 7

O9YNF7 PRELIMINARY; PRT; 257 AA.  
 ID O9YNF7;  
 AC O9YNF7;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9304899;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenhal A., Arcander P., Tjornehoj K., Vinuf B.,  
 Ronved C., Ronsholt L., Alexandersen S., Blixenkron-Moller M.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup: no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptation and passages in cell culture or calves.";  
 RL EMBL; U92100; AAD00712.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne\_attach.  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28324 MW; 94EB8BC358739B8 CRC64;

DR EMBL; U92101; AAD00713.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne\_attach.  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28380 MW; 6BD146B3B02E5ACB CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SPEAKLOPR 14  
 |||||  
 Db 224 SPEAKLOPK 232

## RESULT 8

O9YNF6 PRELIMINARY; PRT; 257 AA.  
 ID O9YNF6;  
 AC O9YNF6;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9314893;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenhal A., Arcander P., Tjornehoj K., Vinuf B.,  
 Ronved C., Ronsholt L., Alexandersen S., Blixenkron-Moller M.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup: no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptation and passages in cell culture or calves.";  
 RL EMBL; U92102; AAD00714.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne\_attach.  
 DR Pfam; PF00802; Glycoprotein\_G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28421 MW; 940C1EB22895BD02 CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SPEAKLOPR 14  
 |||||  
 Db 224 SPEAKLOPK 232

## RESULT 9

O9YNF5 PRELIMINARY; PRT; 257 AA.  
 ID O9YNF5;  
 AC O9YNF5;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=9402020;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenenthal A., Arcander P., Tjørnhøj K., Viuff B.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup; no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptation and passages in cell culture or calves."  
 RL Vet. Microbiol. 62:265-279(1998).  
 DR EMBL; U92103; AAD00715.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 2838 MW; C1A2D35BEC16592E CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 224 SPEAKLOPK 232

RESULT 10  
 Q9YNF4 PRELIMINARY; PRT; 257 AA.  
 AC Q9YNF4; 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 RL Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9402020;  
 RX MEDLINE=99008085; PubMed=9791873;  
 RA Larsen L.E., Uttenenthal A., Arcander P., Tjørnhøj K., Viuff B.,  
 RT "Serological and genetic characterization of bovine respiratory  
 RT syncytial virus (BRSV) indicates that Danish isolates belong to the  
 RT intermediate subgroup; no evidence of a selective effect on the  
 RT variability of G protein nucleotide sequence by prior cell culture  
 RT adaptation and passages in cell culture or calves."  
 RL Vet. Microbiol. 62:265-279(1998).  
 DR EMBL; U92104; AAD00716.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28379 MW; C1A2D36EC16571E CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 224 SPEAKLOPK 232

RESULT 11  
 Q9YS25 PRELIMINARY; PRT; 257 AA.  
 ID Q9YS25

AC Q9YS25; 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 RL Attachment glycoprotein.  
 GN G.  
 OS Bovine respiratory syncytial virus, and  
 OS Bovine respiratory syncytial virus (strain A51908) (BRS).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11246; 11247;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine respiratory syncytial virus; STRAIN=ATUES1908;  
 RX MEDLINE=99102581; PubMed=9847328;  
 RA Buchholz U.J., Finke S., Conzelmann K.K.;  
 RT "Generation of bovine respiratory syncytial virus (BRV) from cDNA:  
 RT BRV NS2 is not essential for virus replication in tissue culture, and  
 RT the human RSV leader region acts as a functional BRV genome  
 RT promoter."  
 RL J. Virol. 73:251-259(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine respiratory syncytial virus; STRAIN=ATUES1908;  
 RA Buchholz U.J., Finke S., Conzelmann K.-K.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine respiratory syncytial virus (strain A51908) (BRS);  
 RX MEDLINE=21580793; PubMed=11724268;  
 RA Yunus A.S., Khatat S.K., Collins P.L., Samal S.K.;  
 RT "Rescue of bovine respiratory syncytial virus from cloned cDNA: entire  
 RT genome sequence of BRSV strain A51908."  
 RL Virus Genes 23:157-164(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine respiratory syncytial virus (strain A51908) (BRS);  
 RA Yunus A.S., Khatat S.K., Collins P.L., Samal S.K.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF992942; AAC96307.1; -.  
 DR EMBL; AF992943; AAL49398.1; -.  
 DR HSSP; P22261; IBRV.  
 DR InterPro; IPR000925; Glycoprot G.  
 DR InterPro; IPR003880; Ppantne attach.  
 DR Pfam; PF00802; Glycoprotein G; 1.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.  
 SQ SEQUENCE 257 AA; 28479 MW; 3AE078372A0FEB1F CRC64;

Query Match 61.4%; Score 43; DB 12; Length 257;  
 Best Local Similarity 88.9%; Pred. No. 5.7;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SPEAKLOPR 14  
 DB 224 SPEAKLOPK 232

RESULT 12  
 Q9XUV5 PRELIMINARY; PRT; 164 AA.  
 AC Q9XUV5; 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 RL k0282.7 protein.  
 GN k0282.7.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lloyd C.R.;

```

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
   investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z81560; CAB04544.1; -.
SQ SEQUENCE 164 AA; 19025 MW; 4208E365751CBCT70 CRC64;

Query Match
Best Local Similarity 58.6%; Score 41; DB 5; Length 164;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 SSFLSPKALQ 13
Db 3 SNFSPKALQ 14

RESULT 13
O9DBT6 PRELIMINARY; PRT; 624 AA.
ID O9DBT6;
AC O9DBT6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 1200014E20R1K protein.
GN TNS OR 1200014E20R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsumoto H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Maehio T.,
RA Sakai K., Orido T., Furuno M., Anon H., Baldarelli R., Barch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004758; BAB23559.1; -.
HSSP; P16277; 1BLK.
MCD; MGI:104552; Tns.
DR InterPro; IPR000050; PID domain.
DR InterPro; IPR000980; SH2-
PFam; PF00017; SH2; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRODOM; PD000093; SH2; 1.
DR SMART; SM00462; PTB; 1.
DR SMART; SM00522; SH2; 1.
DR PROSITE; PSS0001; SH2; 1.
SQ SEQUENCE 624 AA; 65369 MW; 296FC3741EFC57E CRC64;

Query Match
Best Local Similarity 58.6%; Score 41; DB 11; Length 624;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Oy 1 GSSFLSPKALQ 13
Db 31 GSSYNSPDYSLQ 43

RESULT 14
O47732 PRELIMINARY; PRT; 815 AA.
ID O47732;
AC O47732;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE ORF16.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Enterococcaceae; Enterococcus.
OX NCBI_TaxId=1351;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=D816; TRANSPOSON=TN916;
RX MEDLINE=95207419; PubMed=7899523;
RA Piamagan S.E., Zitzow L.A., Su Y.A., Clewell D.B.;
RT "Nucleotide sequence of the 18-kb conjugative transposon Tn916 from
   Enterococcus faecalis."
RL Plasmid 32:350-354(1994).
DR EMBL; U09422; AAB60017.1; -.
SQ SEQUENCE 815 AA; 93317 MW; 594C6A5F4FC59867 CRC64;

Query Match
Best Local Similarity 58.6%; Score 41; DB 2; Length 815;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 SFSPKALQ 12
Db 32 SFSPKALQ 41

RESULT 15
O98F99 PRELIMINARY; PRT; 96 AA.
ID O98F99;
AC O98F99;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein msr3871.
GN MSR3871.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxId=381;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=MAFF30309; PubMed=11214968;
RX Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
   Mesorhizobium loti."
RL DNA Res. 7:331-336(2000).
DR EMBL; AP003002; BAB50668.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 96 AA; 10602 MW; 586EDA57D76BA225 CRC64;

Query Match
Best Local Similarity 57.1%; Score 40; DB 16; Length 96;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

Db 14 GSSMLQPKAELO 25

Search completed: January 29, 2003, 13:23:37  
Job time : 31 secs

---

END PAGE BLANK (USPTO)